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The Scope of Published Population Genetic Data for Indo-Pacific Marine Fauna and Future Research Opportunities in the Region

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research paper

The scope of published population genetic data for Indo-Pacific marine fauna and future research opportunities in the region

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ABSTRACT.—Marine biodiversity reaches its pinnacle in the tropical Indo-Pacific region, with high levels of both species richness and endemism, especially in coral reef habitats. While this pattern of biodiversity has been known to biogeographers for centuries, causal mechanisms remain enigmatic. Over the past 20 yrs, genetic markers have been employed by many researchers as a tool to elucidate patterns of biodiversity above and below the species level, as well as to make inferences about the underlying processes of diversification, demographic history, and dispersal. In a quantitative, comparative framework, these data can be synthesized to address questions about this bewildering diversity by treating species as "replicates." However, the sheer size of the Indo-Pacific region means that the geographic and genetic scope of many species' data sets are not complementary. Here, we describe data sets from 116 Indo-Pacific species (108 studies). With a mind to future synthetic investigations, we consider the strengths and omissions of currently published population genetic data for marine fauna of the Indo-Pacific region, as well as the geographic and taxonomic scope of the data, and suggest some ways forward for data collection and collation.

The waters of the Indian and Pacific oceans contain the greatest concentration of tropical marine biodiversity on Earth (Ekman 1953, Briggs 1974, Veron 1995). The question of why marine biodiversity is concentrated in this region, particularly at the juncture of the Indian and Pacific oceans, has been the topic of much study (Forbes 1856, Ekman 1935, Ladd 1960, Briggs 1974, 1999, Bellwood and Hughes 2001, Connolly et al. 2003, Carpenter and Springer 2005, Hoeksema 2007, Reaka et al. 2008, Renema et al. 2008, Bellwood et al. 2012). Tools from population genetics and phylogeography can enhance our understanding of how biodiversity is created and maintained in this region (Avise et al. 1987, Palumbi 1997, Barber and Bellwood 2005). Moreover, genetic approaches are essential for initial detection of the many cryptic species that apparently exist in this region (Knowlton 2000, Meyer et al.

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2005, Barber and Boyce 2006, Vogler et al. 2008, Bowen et al. 2013) and can also be used to guide conservation (Moritz 1994, Moritz and Faith 2002, Rocha et al. 2007, Beger et al. 2014, von der Heyden et al. 2014).

Numerous studies have investigated population genetic and phylogeographic patterns in the Indo-Pacific region (for examples, see recent reviews by Crandall et al. 2008a, Carpenter et al. 2011, Toonen et al. 2011); however, the high levels of biodiversity, combined with the vast area of the Indian and Pacific oceans, poses substantial challenges for documenting spatial genetic patterns, much less inferring underlying processes. For instance, the coral reefs of eastern Indonesia, Malaysia, the Philippines, Papua New Guinea, East Timor, and the Solomon Islands (collectively referred to as the Coral Triangle), contain the world's greatest concentration of marine species, which is consistently estimated in the upper decile for most coastal marine taxa (Roberts et al. 2002, Carpenter and Springer 2005, Tittensor et al. 2010). Together, the Indian and Pacific oceans span two thirds of the globe, with most individual species ranges encompassing much of one or both ocean basins (Connolly et al. 2003). This area includes more than 65 nations of which 18 are classified by the UN as Least Developed Countries, and only four are classified as High Income Organisation for Economic Co-operation and Development (OECD) countries (http://www.data.worldbank.org, accessed December 2012).

Thus, population genetic surveys in the Indo-Pacific region are likely to involve fieldwork in locations that are distant from each other, potentially difficult to access, may be in developing countries, and will fall under diverse regulations and jurisdictions. These are significant logistical impediments for biological research. Moreover, with such high biodiversity, the degree to which one or a few species can represent entire communities is unknown, and recent studies argue against exemplar species representing patterns for the broader community (Bird et al. 2007, Toonen et al. 2011). In the face of such challenges, progress can be fostered if data are shared and properly catalogued in the interests of capturing emergent patterns in this complex system. Our purpose here is not to provide a review of previous work on genetic patterns in the region (see Palumbi 1994, Benzie 1998, Carpenter et al. 2011, Toonen et al. 2011 for examples focusing on particular regions within the Indo-Pacific). Rather, our goal is to provide a detailed overview of published data from population genetic studies of Indo-Pacific marine fauna, which could be used for synthetic studies. In addition, we aim to inform future empirical studies by determining the scope, strengths, and omissions of collective work to date, considering both the geographic and taxonomic coverage. Finally, we discuss potential uses for these published data that could provide a basis for future synthetic work and suggest guidelines for the collation of such data and future empirical investigations. The 108 studies presented here are the product of many years' work by many researchers and, if consolidated, would provide a solid foundation for our understanding of processes generating biodiversity in the region. Here we attempt to aggregate these efforts, identify significant areas of overlap or gaps, and suggest a standard platform for synthesis and collaboration.

Methods

A literature search was conducted using Web of Science™ (Thomson Reuters) on 21 June, 2012. The search terms were chosen to maximize inclusion of articles

containing georeferenced data on population genetic diversity from shallow water marine habitats in the Indo-Pacific region. The following sets of Boolean search terms were combined in the Advanced Search tool: (1) gene flow OR population structure OR genetic diversity OR phylogeograph* OR F statistic OR mtDNA OR microsatellite OR allozyme, AND (2) Marine OR coral OR reef OR intertidal OR subtidal OR estuar*, AND (3) Indo* OR Malay* OR Indo-Pacific OR Coral Triangle. The titles and abstracts of all papers were assessed and articles that did not fit the following criteria were discarded: (1) only marine animals; (2) only tropical Indo-Pacific studies bounded by the geographical limits of north to Tropic of Cancer (30°N), south to Tropic of Capricorn (30°S), west to Cape Town, South Africa (20°E), and east to the Eastern Pacific Barrier (125°W); (3) only data based on DNA sequences, microsatellites or allozymes; (4) at least three populations were sampled per included study; (5) at least five individuals from a population had to be sampled for that population to be included; (6) the study had to provide sample sizes and indices of genetic diversity at the population level; and (7) the study had to provide latitude and longitude or a map/description of the sampling sufficient to permit location of sampling sites to within 500 km.

Articles remaining in the data set after this first pass were more closely investigated (reading the text of the introduction, methods, results, or supplementary material) to assess their fit to these criteria. Details of the authors, year of publication, genetic marker, sample size, species name, and population geographic positions from articles meeting all criteria were recorded. These criteria targeted population genetic articles, so that purely phylogenetic studies were usually discarded due to low population number or sample sizes. The resulting list was checked by experts in the field attending a catalysis meeting at the National Evolutionary Synthesis Center (NESCent) on the "Molecular Ecology and Evolution of the Indo-Pacific" and some relevant papers not captured by the literature search were added.

All maps were produced in ArcMap (version 10, ESRI, Redlands, CA) using coastline data from the Global, Self-consistent, Hierarchical, High-resolution Shoreline Database (Wessel and Smith 1996). Geographic coverage of studies and species was estimated by measuring the area of a convex hull drawn around the point locations of each study or species. Probability-based species range maps were downloaded from Aquamaps (http://www.aquamaps.org). Sampling locality polygons were generated by buffering each data point by 60 km and dissolving to merge points close to each other. Species range polygons were drawn in ArcMap 10 using a convex hull of the occurrence points listed in the Global Biodiversity Information Facility (GBIF; http://www.gbif.org, accessed 13 November, 2012) supplemented by the genetic database points for each species and some points gleaned from the literature for those species not listed on GBIF. Two species [*Echinometra* sp. C (Uehara and Shingaki 1985) and *Euryhaliotrematoides grandis* (see Appendix 1 for species authorities)] were excluded from these analyses because occurrence data could not be found. The GBIF occurrence polygons were merged and joined with sampling locality polygons to generate a count of species for each locality. We then divided the number of species sampled by the total number from the data set present and converted to a percentage. We chose to standardize by the number of species from the dataset with ranges intersecting a location rather than attempting to derive species richness estimates because reliable estimates of species richness across the six phyla that our data set encompasses are difficult to make. The number of species sampled was also divided by total reef area

within each polygon to generate sampling per unit area of habitat. Statistical analyses were conducted in R statistical software (R Core Team 2012) and areas estimated by convex polygons were square-root transformed prior to analysis. We also performed a community-style cluster analysis using sampling localities as the groups of interest and sampled species as presence/absence information. Thus, inference from this cluster analysis is about sampling practices rather than actual community composition. We calculated Euclidean distances among sites with the vegan package for R (Oksanen et al. 2012) and clustered them into groups using Ward's Minimum Variance criterion.

Results and Discussion

In total, 493 studies were returned from the initial Web of Science search. This number was reduced to 108 following application of the criteria given above (see Appendix 1). These 108 studies covered 116 species in six phyla. The data set contained 1451 genetic diversity data points, with each point representing a georeferenced collection of a given species (five or more individuals of that species) and genotyped by a category of marker (mtDNA sequencing, microsatellites, or allozymes). In the final data set, there were 725 different geographic locations in 50 different countries.

Taxonomic Patterns.—Among Indo-Pacific genetic studies, there was a clear bias toward ray-finned fishes; just over half (69 of 126) of all species studied were Actinopterygians. The remaining 57 studies surveyed were, in descending order of coverage: Mollusca (16 species), Arthropoda (11 species), Echinodermata (11 species), Cnidaria (4 species), other Chordata (2 species of reptile, 2 species of shark and 1 species of lancelet), and a single representative of the Platyhelminthes (Fig. 1). Thus, large and relatively firm-bodied taxa have been preferred, whereas speciose phyla such as Annelida, Cnidaria, and Porifera have been overlooked, perhaps due to difficulty in identification, preservation, or subsequent DNA amplification. Even the relatively well-studied Mollusca were under-represented in comparison to fishes when considering their proportional species richness in marine habitats [more than 40,000 estimated species of molluscs (WoRMS Editorial Board 2012) vs 16,764 of Actinopterygians (Eschmeyer et al. 2010)].

This large discrepancy in studies across phyla does not simply result from investigator bias. Invertebrates are generally more difficult to identify to the species level for the non-expert and molecular work is often challenging due to a paucity of genomic information for primer design (Toonen 1997, Fernandez-Silva et al. 2013). In addition, mucus and other polysaccharides commonly found in marine invertebrates are known to inhibit PCR (Huelsken et al. 2011, Vargas et al. 2012). Finally, anthozoans and sponges have a notorious deficiency of variation in their mitochondria (Shearer 2002, Hellberg 2006), such that this useful genetic marker is usually not informative for these taxa (but see Forsman et al. 2009), and development of nuclear markers has generally lagged far behind mtDNA (Karl and Avise 1993, Hare 2001, Puritz et al. 2012). Conversely, fishes are good candidates for population genetic and phylogeographic studies due to their varied life histories and functional traits and their many readily identifiable species. Genetic work tends to be easier in fishes, whose vertebrate affiliation and economic importance mean that there is a plethora of genetic information available for primer design. Despite this overall skew towards fishes,

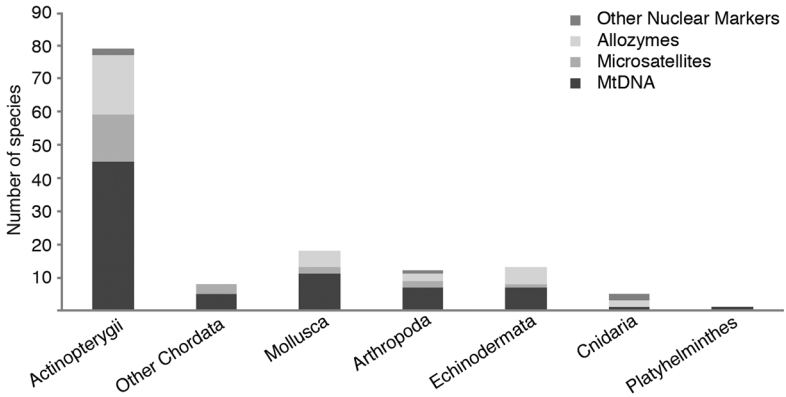


Figure 1. Histogram showing the number of taxa studied by the four categories of molecular marker type.

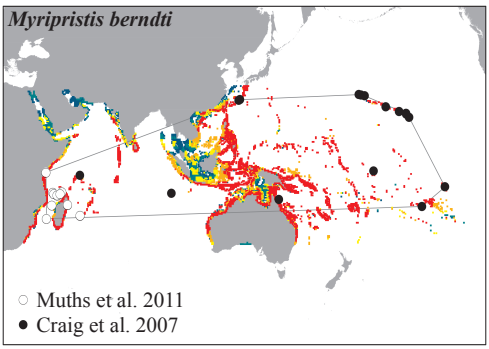
however, the top five most studied species in this data set (based on the number of published studies of that species and by the number of total geographic locations sampled for each species) consisted of four invertebrates and a single fish (discussed in detail in the Text Box, *see next page*).

The bias toward Actinopterygii remains in multi-species studies. There are 19 studies in the final data set that include more than one species, of which 12 were of fishes (Doherty et al. 1995, Dudgeon et al. 2000, Fauvelot and Planes 2002, Drew et al. 2008, Magsino and Juinio-Meñez 2008, Ramon et al. 2008, Thacker et al. 2008, van Herwerden et al. 2009a, Gaither et al. 2010, Mirams et al. 2011, Lord et al. 2012, Ludt et al. 2012) and seven of invertebrates (Palumbi et al. 1997, Uthicke et al. 2001, Barber et al. 2002, Crandall et al. 2008a,b, Kochzius et al. 2009, Duda et al. 2012). Generally, studies include phylogenetically similar species (e.g., for fishes: Fauvelot and Planes 2002, Magsino and Juinio-Meñez 2008, Thacker et al. 2008, Lord et al. 2012, Ludt et al. 2012; and for invertebrates: Palumbi et al. 1997, Uthicke et al. 2001, Barber et al. 2002, Crandall et al. 2008a, Duda et al. 2012). However, an exception is that two multispecies studies have focused on the seastar *Linckia laevigata* and its gastropod parasite *Thyca crystallina* (Crandall et al. 2008b, Kochzius et al. 2009). The comparative context that is offered by multi-species studies is valuable to any attempt to establish general associations between genetic patterns and geography or biological traits (Bowen et al. 2014). It is hoped that future sampling efforts can be coordinated in such a way as to maximize the comparative value of data sets for individual species (see below).

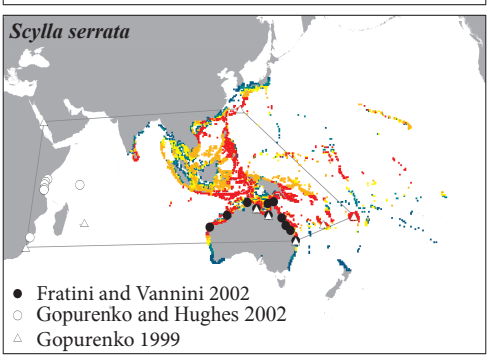
Geographic Scope.—Given the vast area and logistical constraints to fieldwork in the Indo-Pacific, it is not surprising that few Indo-Pacific genetic studies encapsulate the entire geographic range of a species. We examined the geographic scope of studies using a variety of criteria: the geographic extent (area encompassed by sampling), the number of sampling sites, and the density of sampling locations within geographic extent (Fig. 2). The five species with the greatest geographic sampling extent are highlighted in the Text Box. A general perception of population genetic studies is that there is an inherent trade-off between the geographic extent of sampling and the number of sampling sites. That is, some sampling strategies might be expected to include geographically distant sites to maximize the geographic extent

▼ The top five species with greatest sampling extent

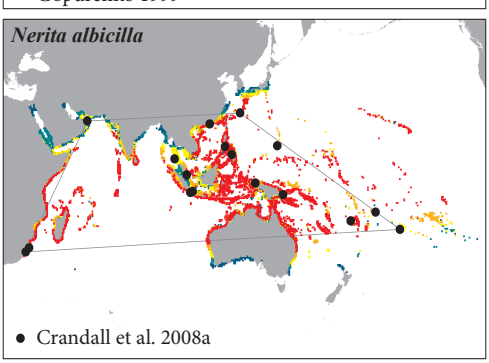
Species sampled across a wide area represent those for which broadscale patterns can be investigated. Heatmap colours show probabilistic occurrence from Aquamaps.org. Symbols show sampling events.



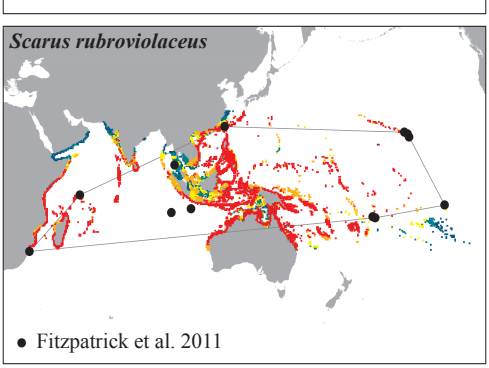
Myripristis berndti, the bigeye soldierfish, is the species with the widest geographic coverage. The species has been the focus of two population genetic studies: one study restricted to sites around Madagascar (Muths et al. 2011) using mtDNA (*cytochrome oxidase b*) and microsatellites and one study with sites in both the Indian and Pacific Oceans (Craig et al. 2007) using mtDNA (*cyt b*) alone, yet neither study included locations in the Coral Triangle. Extending future coverage to include the Coral Triangle would be an obvious next step for this species.



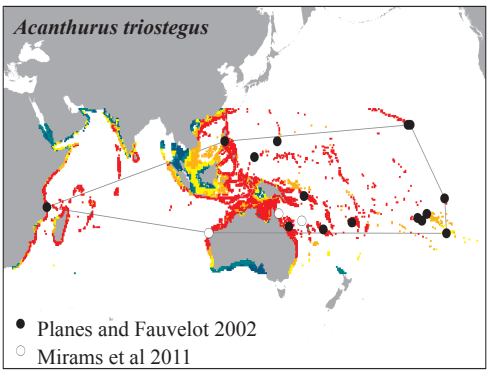
Scylla serrata, the mud crab, ranks second in the greatest geographic sampling extent. It has been the focus of three Indo-Pacific studies (Gopurenko 1999, Fratini and Vannini 2002, Gopurenko and Hughes 2002). Each employed mtDNA *COI*, so combination of the data is straightforward. For this reason, further studies on this species should include *COI* sequencing. With the exception of the Solomon Islands [Liu et al. 2007 (not captured by this search, part of a synthesis by Fratini et al., 2010)], there are no data for *S. serrata* from the Coral Triangle.



Nerita albicilla, an intertidal gastropod, is the species with the largest geographic coverage represented by a single study. Crandall et al. (2008a) included the species alongside its congener *Nerita plicata* in a comparative study that revealed markedly different patterns of genetic structure between these two closely related and ecologically similar species. It would seem that the majority of the species range has been covered by this study (and by Frey and Vermeij 2008, although this study was excluded from the dataset as it did not report genetic diversity data).



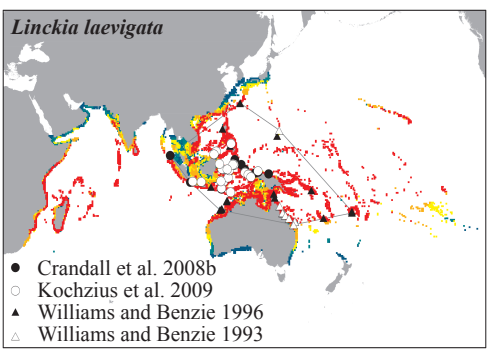
Scarus rubroviolaceus, the redlip parrotfish, has been surveyed from South Africa to the Marquesas within a single study. Fitzpatrick et al. (2011) used patterns of genetic structure in this species to distinguish between hypotheses explaining the diversity hotspot found in the Coral Triangle. The sampling in this study covered the edges of the species range fairly well, with the exception of the Coral Triangle itself. Sites in the Coral Triangle would enhance the understanding of processes behind patterns of high diversity at the juncture between the Indian and Pacific oceans.



Acanthurus triostegus, the convict surgeonfish, has a range spanning the Indian and Pacific oceans. This is the fifth widest sampled species included, with 7879 km^2 covered by two studies. Planes and Fauvelot (2002) used allozymes to assess population structure in the Pacific Ocean, but sampled only a single location in the Indian Ocean and none in the Coral Triangle. Mirams et al. (2011) used mtDNA (*COI*) to investigate the effect of the Torres Strait landbridge, sampling two sites in the Pacific Ocean and one in the Indian Ocean. The different molecular markers preclude combination of existing data, but there is scope for further sampling of the Indian Ocean and Coral Triangle.

▼ The top five species with the most locations sampled

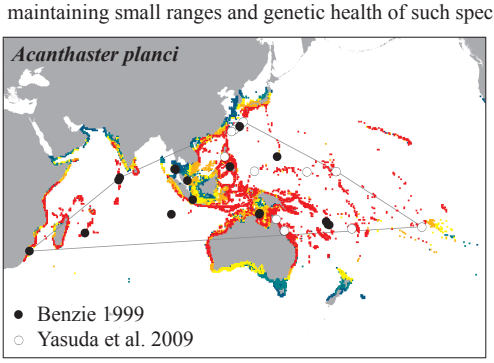
Species sampled from the highest number of locations represent those that may be a potentially fruitful focus for more geographically widespread sampling, even if individuals studies did not encompass a wide expanse of the ocean.



Linckia laevigata, the blue starfish, has been the focus of four studies covering 59 sites. *Linckia laevigata* and its parasite *Thyca crystallina* (Crandall et al. 2008b, Kochzius et al. 2009) were included in two mtDNA *COI* studies in the Coral Triangle. Two allozyme studies (Williams and Benzie 1993; 1996) sampled more widely, however there remains scope for work across the Indian and Pacific Oceans. Further work should include *COI* to allow data combination. A recent study has made a start on addressing this gap with *COI* sequences from Kenya and Madagascar (Otwoma 2012).

Scylla serrata, the mud crab, has been both densely and widely sampled (map shown opposite page). The density is due to it having been the focus of two fine scale studies in different oceans (Fratini and Vannini 2002; Gopurenko and Hughes 2002), which drives up the sampling location numbers and area of the species sampling polygon. There remains scope for further work on this species in the region.

Pterapogon kauderni, the Banggai cardinalfish (map not shown), is endemic to Indonesia and Malaysia. It has been the focus of three studies (Bernardi and Vagelli 2004, Hoffman et al. 2005, Vagelli et al. 2009) over most of its range, each using different markers. Further studies on other endemics could reveal mechanisms maintaining small ranges and genetic health of such species.



*Acanthaster planci***,** the Crown of Thorns seastar, has been studied twice in the Indo Pacific (Benzie 1999, Yasuda et al. 2009) at 36 locations. The sampling of the above studies overlaps in the west Pacific but coverage is lacking in the rest of the Pacific. This gap is partially filled by two recent mtDNA papers in the Central Pacific (Timmers et al. 2011, 2012); however, the addition of mtDNA (*control region*) work on this species from the Indian Ocean and Coral Triangle would allow combination of these data.

Tridacna crocea, the boring giant clam, has been the focus of two studies at 35 sites in the Coral Triangle (DeBoer et al. 2008; Kochzius and Nuryanto 2008). Coverage in this region is substantial, but absent elsewhere in the species' range. There is wide opportunity for further work on *T. crocea*, particularly using mtDNA *COI* to fit with existing work and increase the geographic scope.

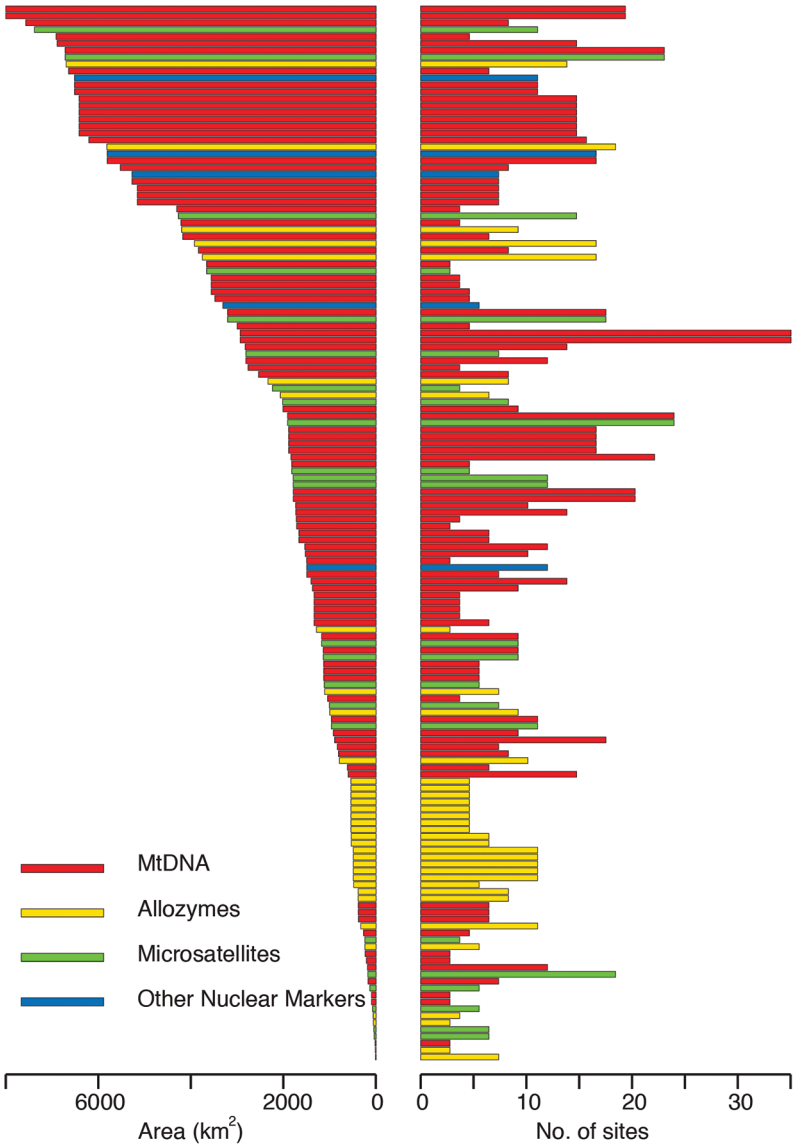


Figure 2. Summary of sampling for genetic surveys included in the present study. Total area surveyed (km^2) and the number sites survey are indicated per species.

of the study but that the expense and logistics of widespread sampling would limit the total number of sites. Other studies might prioritize sampling density and limit themselves to a smaller geographic extent but include more total sites. In addition, it could be that studies of the latter type might preferentially use microsatellites so as to infer recent migration events.

These expectations, however, were not borne out. The area encompassed by individual studies varies widely from 14.8–9092 km^2 (with mean and median values of 2141 and 1892 km^2) and the maximum number of sites is 38 (with a mean and median of 10.4 and 9 per study). There was a slight but significant positive relationship

between sampling area (i.e., geographic extent) and number of sites (that can be described by the equation: no. sites = 5.648 + 0.102 (√ area), $F_{1,150} = 24.96$, $R^2 = 0.143$, $P < 0.00001$, following removal of an outlier study (Johnson et al. 1994), which included eight sites over approximately 14 km^2. Sampling areas differ according to the genetic marker employed by each study (ANOVA: $F_{3,149} = 8.94$, $P < 0.0001$), with the greatest geographic extent for studies using "other" nuclear markers, followed by mtDNA sequences, microsatellites, and allozymes. The difference in area is only significant when comparing allozyme studies to either mtDNA sequence or "other" nuclear marker studies (Tukey's post hoc tests: both $P < 0.004$). Thus, contrary to expectations, there was no significant difference in sampling area between microsatellite and mtDNA based studies. The number of sites surveyed had no effect on the choice of genetic marker (ANOVA: $F_{3,149} = 1.075$, $P = 0.361$). In summary, then, there was no evidence for trade-offs between sampling extent and number of sites among Indo-Pacific studies.

Two noteworthy studies illustrated the lack of inverse correlation between geographic extent of sampling and density of sampling locations. First, the study with the greatest geographical extent (9092 km^2) explored the phylogeographic patterns of *Nerita albicilla* and *Nerita plicata*, two intertidal gastropods (Crandall et al. 2008a) and included a number of evenly-spaced sites (21 sites included in this database) spanning most of the species' range (see Text Box). Second, the study with the maximum number of sampling locations (38 sites) encompassed 3336 km^2 of the Coral Triangle and provided comparative data for two closely related species of mantis shrimp (Barber et al. 2002). These two studies have both managed to achieve substantial geographic coverage alongside maintaining a high number of sampling locations and focusing on more than one species.

Another aspect of geographic sampling scope concerns the total number of sampling locations, especially combined across multiple studies. Species that have been included in multiple studies represent opportunities for collaboration and data synthesis, whereby the total geographic scope could be maximized. The five species with the greatest total number of sampling locations are discussed in the Text Box and represent opportunities for synthetic analyses. An extension of the total number of sampling locations is the density of sampling per species (total area covered / number sampling locations). While species with wide geographic sampling covering substantial portions of their range are important for revealing broadscale phylogeographic patterns, studies with dense sampling provide detailed knowledge of connectivity in a small area that may be particularly relevant to marine conservation management actions (Harrison et al. 2012). The top five species in terms of the density of sampling points were: *Craterocephalus capreoli, Pterapogon kauderni, Siganus guttatus, Chromis atripectoralis,* and *Stegastes nigricans.* Such data sets can complement wide-ranging data sets by illuminating population genetic patterns at a small scale but the direct applicability of their findings is necessarily limited to the region in question.

Identifying Anchor Locations.—Given the many difficulties associated with field work in the Indo-Pacific region, it might be expected that researchers would choose to sample in places they or colleagues have sampled before, that are easy to access, or might have colleagues collect for them to reduce the costs. These locations might be established marine stations run by universities or non-governmental

organizations, or they may simply be places where a "pioneer" researcher has established a connection and opened up the way for other researchers to follow. This would lead to a pattern of a few sites being the focus of multiple studies on multiple species. From the perspective of future work in the region, such sites can provide "anchor" locations with which direct comparisons can be made among taxa and studies, and therefore their inclusion might be prioritized in future empirical research projects.

Most of the point locations sampled to date were represented for only one species (484 locations out of a total of 682 locations) or by one study (490 locations); however, several localities stand out for the number of species sampled there. Localities are defined here as the polygons created by buffering each data point by 60 km and dissolving to merge points close to each other into a single locality. Figure 3 illustrates these patterns of uneven sampling across the Indo-Pacific region. Figure 3A shows localities colored according to the number of species that have been sampled as a proportion of those species in the data set with ranges intersecting that locality. The Society Islands, the Marquesas, and Main Hawaiian Islands in the central Pacific are localities where sampling has been high relative to the number of species occurring there (>40% of species from the dataset have been sampled). Other potential "anchor" localities identifiable from Figure 3A are the Northern Great Barrier Reef (GBR), Okinawa, Marutea Atoll in the central Pacific, and Pearl and Hermes Atoll in the Northwestern Hawaiian Islands. However, when the percentage of species sampled in a locality is divided by the area of the locality polygon, we can see patterns of coverage per unit area (Fig. 3B). After this correction has been made, Rangiroa, Takapoto, and Kiritimati in the central Pacific, along with the Seychelles, Christmas Island, and Cocos-Keeling Island in the Indian Ocean emerge as important nodes. Not surprisingly, the GBR localities fade in their influence due to the large area they encompass. Nevertheless, the dense sampling within the GBR, as evidenced by the sizes of the polygons resulting from buffering of point locations, and the relative ease of accessibility of remote reefs here, argues for its inclusion in any list of target locations.

Co-sampled Localities.—The above section illustrates that sampling effort has been uneven across the Indo-Pacific region, with some locations attracting more sampling events than others. Here we investigate whether certain sites are commonly co-sampled, such as might be expected from a situation of reusing the same anchor locations, combining the sampling of many species in a single sampling expedition, or planned multispecies investigations. Figure 4 shows this tendency for subsets of locations to be co-sampled across species. The Hawaiian islands locations form a single cluster (yellow in online version) reflecting the many studies that have sampled multiple locations within Hawaii. Similarly, sites from the Coral Triangle form a distinct cluster (blue in online version). The Great Barrier Reef (green in online version) is strikingly unconnected to other localities, indicative of many studies that have sampled within the GBR only and not included additional locations. Conversely, a suite of isolated oceanic islands from both the Pacific and Indian oceans (red in online version) have been intensely co-sampled despite their geographic breadth (the Seychelles to the Marquesas, >165° of longitude).

These clusters of sampling effort highlight opportunities for multispecies syntheses (within sampling blocks), but also show how the currently available data limit

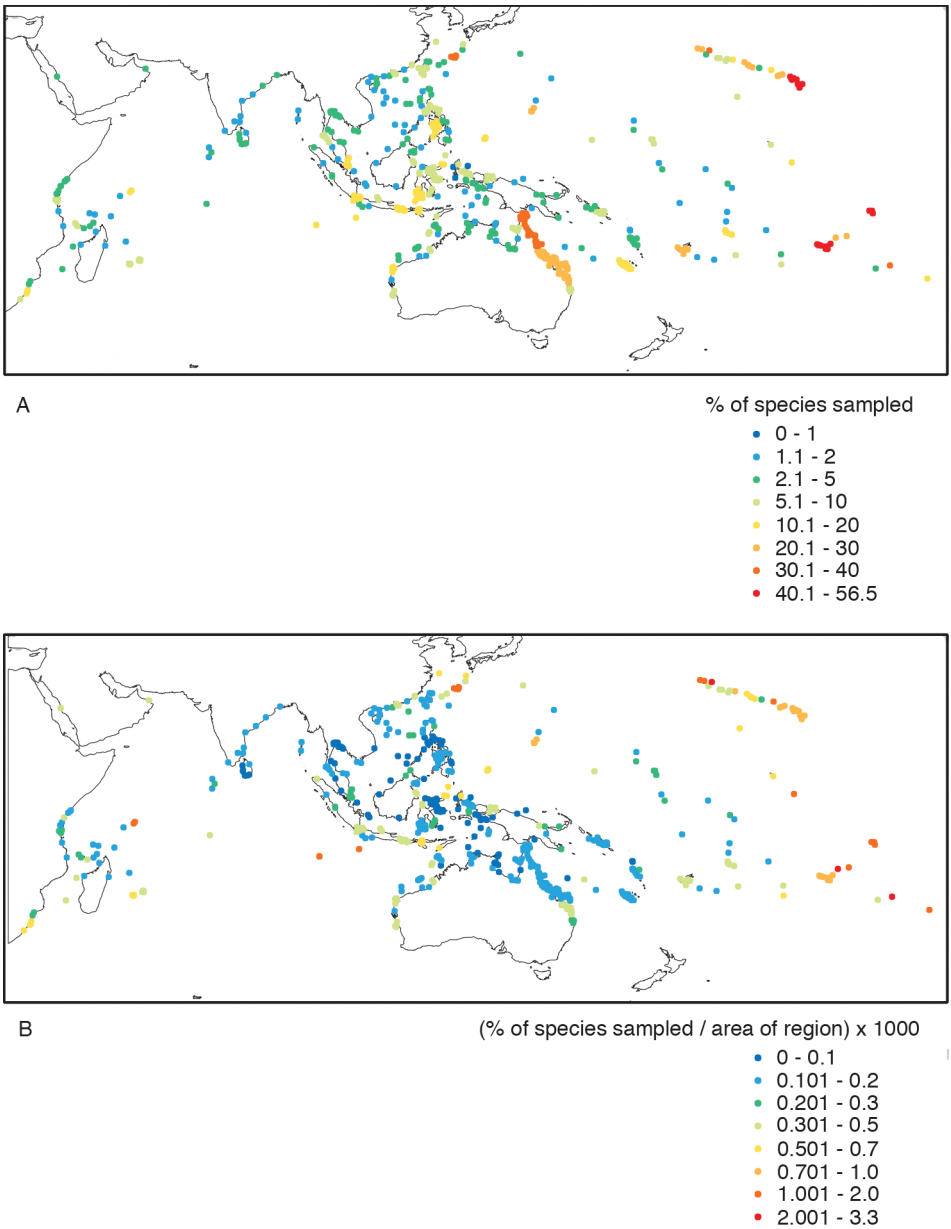


Figure 3. (A) Sampling intensity for the 116 species surveyed. A heatmap colored by the proportion of studied species is shown per site with a correction for species range. For example, from the main Hawaiian Islands, 22 species have been surveyed and 39 species from the 116 in the data set have species ranges that encompass this location, which gives a percentage of 56.4. (B) Sampling intensity for the 116 species corrected for the area of the study locality. As the locality polygons are of different area depending on the proximity of sampling locations, this correction allows us to see intensity of sampling per unit area. For example, the Main Hawaiian Islands locality has an area of 69,063 km^2, so the corrected sampling intensity is 56.4 / 69,063 or 0.0008.

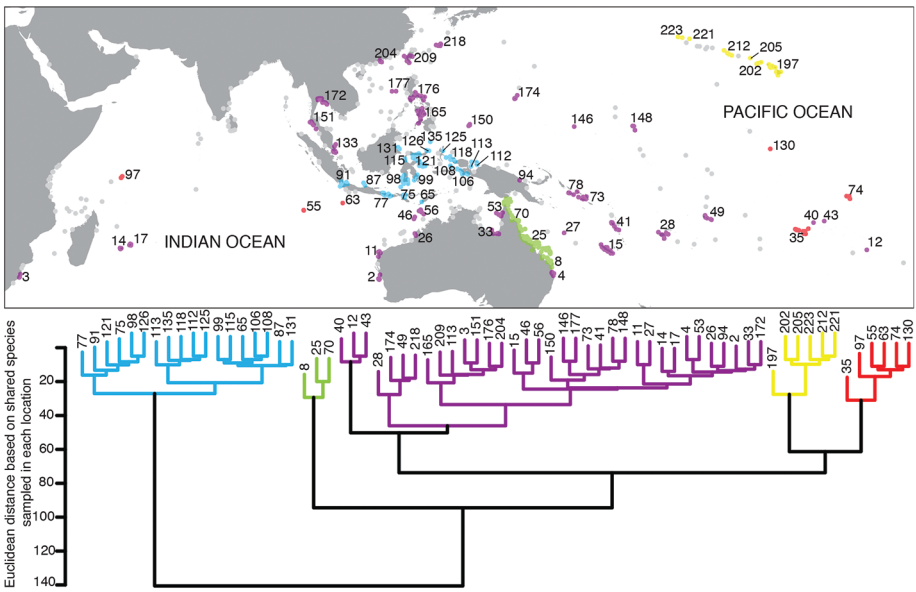


Figure 4. Analysis of species co-sampling. Cluster dendrogram is based on squared Euclidean distances among sampling localities, derived from the composition of species that have been co-sampled in each locality. Localities with a higher number of co-sampled species have a lower Euclidean distance between them. Colors in online version show the geographic spread of clusters of co-sampled localities across the Indo-Pacific region. Only localities where more than five species have been surveyed are shown on the map.

our ability to make inferences on an oceanic scale. For example, whereas there has been strong sampling effort in the highly biodiverse Coral Triangle (blue in online version of Fig. 4), these results cannot be directly compared to other localities due to a tendency not to co-sample species. Designing future empirical work to link clusters would greatly enhance broadscale geographic inferences, for instance future species sampling from oceanic islands (red in online version) that targeted well-sampled species from the Coral Triangle (blue in online version) or vice versa, would permit direct comparisons between core and peripheral locations. Some sampling clusters may be driven by certain species only occurring in restricted areas (e.g., endemics), especially Hawaii. The lack of locational co-sampling involving the GBR is noteworthy given the geographic proximity of the GBR to other high profile regions (namely, the Coral Triangle and west Pacific) and its importance as a World Heritage Site.

Mitochondrial Sequencing and Prospects for Combining Data.—Mitochondrial DNA sequences have been the markers of choice for genetic studies in the Indo-Pacific region (Fig. 1). For studies of invertebrates, mitochondrial COI is clearly the locus of preference (with 28 of 30 studies using COI). For chordates, including bony fishes, there is a greater diversity of target loci, with mitochondrial control region being the most common (32 studies), followed by mitochondrial cytochrome b (17) and cytochrome oxidase subunit I (COI) (12). Thus, a researcher embarking on a genetic survey of a chordate would be well advised to determine with which marker previous work has been conducted on their focal species and pick a target locus accordingly.

Sequence based markers are especially amenable for combining data sets, provided that different studies target the same locus. Markers based on fragment size or charge differences (microsatellites and allozymes, respectively) are not directly comparable across research groups without sharing standards (such as tissues genotyped by each group to form a common frame of reference). Therefore, microsatellite and allozyme studies are often limited to stand-alone examples of genetic patterns for a particular species. Regardless of the marker used, qualitative patterns of divergence can be recognized, however, quantitative analyses rely on data produced from the same marker to control for different mutation rates. Sequence data can be exchanged with fewer concerns about reliability, and most studies currently upload their edited sequences to public repositories [e.g., NCBI Genbank (http://www.ncbi.nlm.nih.gov/genbank), EMBL-Bank (http://www.ebi.ac.uk/embl), and the DNA Data Bank of Japan (http://www.ddbj.nig.ac.jp)]. Thus, the growing collection of mtDNA sequence data is a valuable public resource for the Indo-Pacific research community. However, these data are most useful to other researchers when properly georeferenced (see best practice recommendations below). As a measure of the current standard of georeferencing, 20 studies were excluded from the data set owing to vague reporting of geographical locations. If a population sampling location could not be identified to within approximately 500 km the location was excluded from the dataset; this resulted in 19 data points covering nine species in 10 localities being excluded from the set of accepted studies.

The emergence of several DNA barcoding initiatives in recent years has led to the gathering of large volumes of mtDNA sequence data for the purposes of identification and cataloguing of biodiversity. DNA barcoding involves the sequencing of a common gene that is informative of species-level differences; the accepted barcode for most animals is a fragment of the mitochondrial COI gene. Global marine barcoding projects include Barcode of Life Datasystems (BOLD), Tree of Life, FishBOL, MarBOL, CnidToL, and the Sponge Barcode Project. When the data from these initiatives are made public, they will greatly increase the geographic and taxonomic scope of available mtDNA COI data. This further argues for the inclusion of this locus in population genetic studies in the region.

Recommendations for Future Work

Data Synthesis as an Approach for Understanding Indo-Pacific Biodiversity.—Greater knowledge regarding the spatial genetics of Indo-Pacific taxa will inform long-standing questions regarding the origin and dynamics of marine biodiversity in the Indian and Pacific oceans. Simply put, these oceans are far too large and their communities far too diverse for any single research group to empirically summarize spatial genetic diversity. Only by combining data across locations and taxa can broadscale emergent patterns be identified. For instance, where are the geographic locations of genetic disjunctions and how do they differ among species? Are there biological traits that influence the permeability of a barrier to gene flow? In the Coral Triangle, at the juncture of the Indian and Pacific oceans, there appear to be many instances of genetic breaks (Carpenter et al. 2011), but how such barriers differ among taxa is poorly resolved. Conversely, within the Hawaiian Archipelago, concordant genetic breaks are observed across broad taxonomic lines that are not obvious from any of the single-species studies to date (Toonen et al.

2011). Competing hypotheses regarding broadscale patterns of species diversity (Bellwood et al. 2012) invoke asymmetric migration or colonization. Population genetics provides tools to estimate these asymmetries and this could be done for many taxa. While the main objective of the present study has been toward compiling studies listing genetic diversity data, the practice of using phylogenies combined with information about range size and location alongside species traits has been gaining ground in recent years (Meyer 2003, Paulay and Meyer 2006, Selkoe et al. 2010, Choat et al. 2012). These recent papers provide examples of the kind of synthetic work that can be done with existing data to make sense of the bewildering array of biodiversity in the Indo-Pacific region.

Traditional population genetic reviews have been based on qualitative assessment of published works, which are being complemented by a growing literature using quantitative tests of specific hypotheses (examples from the Indo-Pacific region include: Meyer 2003, Lessios and Robertson 2006, Paulay and Meyer 2006, Hickerson and Meyer 2008, Crandall et al. 2012), and some rely upon reusing previously published data (Bradbury and Bentzen 2007, Weersing and Toonen 2009, Mirams et al. 2011, Riginos et al. 2011, Selkoe and Toonen 2011). Multiple-species studies are essential for addressing questions about how geography and biological traits affect genetic diversity and partitioning, as species are the unit of replication. Concordant patterns among species support scenarios whereby shared geographic features contribute to similar population genetic structure (Avise 2000), and comparisons among closely related taxa can reduce evolutionary variance when searching for commonalities or points of contrast between species (Dawson 2012). Many research programs are purposefully co-sampling numerous taxa, although the theory for simultaneous statistical evaluation of multiple species is not well developed (see Hickerson and Meyer 2008 for an important exception and example).

Thus, the potential value of any single study exceeds one or two standalone publications. The value of such data synthesis is becoming apparent across the fields of ecology and evolutionary biology and, concurrently, a cultural shift is underway whereby many funding bodies (including the National Science Foundation in the USA, the National Environment Research Council in the UK, and the Deutsche Forschungsgemeinschaft in Germany) and journals (see http://www.datadryad.org/pages/jdap for a list of journals in evolution and ecology) are requiring that raw data be accessible. Ensuring raw data are made public provides direct benefits to the scientific community, including long-term preservation, verifiability, and availability for data reuse (Tenopir et al. 2011, Whitlock 2011), and also to the publishing author, as citation rates are higher for papers that make their data available (Whitlock 2011). Despite this apparent shift, there are no official guidelines or consensus as to what constitutes essential data elements for population genetics so that what is reported across studies varies widely.

Best Practices for Reporting Population Genetic Data.—Here, we outline the minimal scope of a population genetic survey and the aspects of data that should be reported for Indo-Pacific studies to maximize the continued utility of published work to the scientific community. We recommend that a population genetic survey include an absolute minimum of three populations to allow partitioning of diversity among locations. Whereas in this survey we include studies sampling as few as five individuals per population in the interests of representing a full range of studies, we

believe that targets of at least 15 individuals per population for mitochondrial sequence data and 20 for microsatellites and SNPs would provide reasonable estimates of diversity by location. Data reporting should include the latitude and longitude of each sampled population with a detailed map as a beneficial complement. Dates of collections are essential to allow the consideration of temporal change.

In addition to the sample size and exact sampling locations, our opinion is that a population genetic study should report frequently used summary statistics that provide commonality across studies. This includes reporting diversity per location [haplotype diversity (h) and average pairwise differences (π) for sequence data, allelic diversity/number of alleles (A) for microsatellites, minor allele frequency for SNPs, and both observed (H_O) and expected (H_E) heterozygosity for genotype data]. Authors should also report measures of population differentiation (with *F*-statistics being the most commonly reported differentiation statistics). Although reporting of *F*-statistics has differed based on data type (G_{ST} and similar statistics being used for genotype data, and N_{ST} statistics for sequence data), recent work has identified the need to consider allelic diversity (Hedrick 2005) so that metrics correcting for this diversity might be in order (see Bird et al. 2011 for an extended discussion). Neutrality test scores for sequence data are also useful, with Tajima's D and F_S (Tajima 1989, Fu 1997) being commonly used, though there is disagreement about the suitability of current null models for mitochondrial sequence data (Wares 2009). If nothing more, the diversity of possible estimators underscores the necessity of making all raw data available so that new approaches can be applied to old data.

Edited, georeferenced sequence data of unique haplotypes should be accessioned at NCBI, EMBL, or DDBJ and accession numbers reported. Unedited, georeferenced sequences (e.g., FASTA files) for all individuals, along with input files for all reported statistics (e.g., NEXUS, XML, or .parm files, etc.), should be deposited in a flexible online data repository such as Dryad (http://www.datadryad.org) for studies to be fully transparent and repeatable. Many studies (examples include work from some of the authors on this paper) only take partial steps toward such accessioning, such as depositing sequences of unique haplotypes only or labeling accessions in a manner whereby the geographic origins are unclear.

For multilocus genotype data, ideally full genotypes of all individuals should be made available and their geographic origins explicit. However, there is no easily searchable public repository designed for such data at present. The creation of a shared database including all Indo-Pacific population genetic data would allow such data to be housed and, if integrated with a collaborative online research forum, would facilitate further progress in the field. Until such infrastructure exists, placing full georeferenced genotype information in Dryad or appending files as supplements to the published paper would represent best practice. Because sequence data, especially from mtDNA, can be readily consolidated among research groups (see previous section), there is a distinct advantage to including mtDNA sequences as part of all future genetic surveys.

While the above practices will help maintain consistency across population genetic studies and facilitate collation of data, sampling for these studies also yields data useful to users outside the field of molecular ecology. For example, the locations of sampled populations can add data to occurrence databases for the species, allowing refinement of species range maps and the mapping of species richness patterns. At present, there is a notable mismatch between the locations of occurrence data points

held in GBIF and those for the same species from population genetic studies; this can be easily solved by integrating these useful online repositories.

The recommendations laid out in this final section are likely to be familiar to most readers; we are not suggesting a major shift, merely a strengthening of the system already in place and the potential addition of more streamlined workflows. In an age where genetic data are increasingly numerous and funding agencies are increasingly frugal, we have a responsibility to make the most out of the existing data, compile new data in easily accessible ways and foster collaborative synthesis across regions with a view to tackling some of the "big" questions regarding marine biodiversity in the Indo-Pacific region.

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Literature Cited

Antoro S, Na-Nakorn U, Koedprang W. 2006. Study of genetic diversity of orange-spotted grouper, *Epinephelus coioides,* from Thailand and Indonesia using microsatellite markers. Mar Biotechnol. 8(1):17–26. PMid:16331343. http://dx.doi.org/10.1007/s10126-005-5026-0

Avise JC. 2000. Phylogeography: the history and formation of species. Cambridge, MA: Harvard University Press.

Avise JC, Arnold J, Ball RM, Bermingham E, Lamb T, Neigel JE, Reeb CA, Saunders NC. 1987. Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. Annu Rev Ecol Syst. 18:489–522.

Barber P, Boyce SL. 2006. Estimating diversity of Indo-Pacific coral reef stomatopods through DNA barcoding of stomatopod larvae. Proc Roy Soc London Ser B-Biol Sci. 273(1597):2053–2061. PMid:16846913. PMCid:PMC1635474. http://dx.doi.org/10.1098/rspb.2006.3540

Barber PH, Bellwood DR. 2005. Biodiversity hotspots: evolutionary origins of biodiversity in wrasses (Halichoeres: Labridae) in the Indo-Pacific and new world tropics. Mol Phylogenet Evol. 35(1):235–253. PMid:15737594. http://dx.doi.org/10.1016/j.ympev.2004.10.004

Barber PH, Moosa MK, Palumbi SR. 2002. Rapid recovery of genetic populations on Krakatau: diversity of stomatopod temporal and spatial scales of marine larval dispersal. Proc Roy Soc London Ser B-Biol Sci. 269(1500):1591–1597. PMid:12184829. PMCid:PMC1691063. http://dx.doi.org/10.1098/rspb.2002.2026

Bastidas C, Benzie JAH, Uthicke S, Fabricius KE. 2001. Genetic differentiation among populations of a broadcast spawning soft coral, *Sinularia flexibilis,* on the Great Barrier Reef. Mar Biol. 138(3):517–525. http://dx.doi.org/10.1007/s002270000480

Bastidas C, Benzie JAH, Fabricius KE. 2002. Genetic differentiation among populations of the brooding soft coral *Clavularia koellikeri* on the Great Barrier Reef. Coral Reefs. 21:233–241.

Bay LK, Choat JH, van Herwerden L, Robertson DR. 2004. High genetic diversities and complex genetic structure in an Indo-Pacific tropical reef fish (Chlorurus sordidus): evidence of an unstable evolutionary past? Mar Biol. 144(4):757–767. http://dx.doi.org/10.1007/s00227-003-1224-3

Beger M, Selkoe K, Treml E, Barber PH, von der Heyden S, Crandall E, Toonon RJ, Riginos C. 2014. Evolving coral reef conservation with genetic information. Bull Mar Sci. 90:159–185. http://dx.doi.org/10.5343/bms.2012.1106

Bellwood DR, Hughes TP. 2001. Regional-scale assembly rules and biodiversity of coral reefs. Science. 292(5521):1532–1535. PMid:11375488. http://dx.doi.org/10.1126/science.1058635

Bellwood DR, Renema W, Rosen BR. 2012. Biodiversity hotspots, evolution and coral reef biogeography: a review. *In:* Gower D, Johnson K, Richardson R, Rosen B, Rüber L, Williams S, editors. Biotic evolution and environmental change in southeast Asia. Cambridge, UK: Cambridge University Press. http://dx.doi.org/10.1017/CBO9780511735882.011

Benzie J. 1998. Genetic structure of marine organisms and SE Asian biogeography. *In:* Hall R, Hollway JD, editors. Biogeography and geological evolution of SE Asia. Kerkwerve, the Netherlands: Backhuys Publishers. p. 197–209.

Benzie JAH. 1999. Major genetic differences between crown-of-thorns starfish (*Acanthaster planci*) populations in the Indian and Pacific oceans. Evolution. 53(6):1782–1795. http://dx.doi.org/10.2307/2640440

Benzie JAH, Williams ST. 1995. Gene flow among giant clam (*Tridacna gigas*) populations in Pacific does not parallel ocean circulation. Mar Biol. 123(4):781–787. http://dx.doi.org/10.1007/BF00349121

Benzie JAH, Williams ST. 1997. Genetic structure of giant clam (*Tridacna maxima*) populations in the west Pacific is not consistent with dispersal by present-day ocean currents. Evolution. 51(3):768–783. http://dx.doi.org/10.2307/2411153

Bernardi G, Vagelli A. 2004. Population structure in Banggai cardinalfish, *Pterapogon kauderni,* a coral reef species lacking a pelagic larval phase. Mar Biol. 145:803–810.

Bird CE, Holland BS, Bowen BW, Toonen RJ. 2007. Contrasting phylogeography in three endemic Hawaiian limpets (*Cellana* spp.) with similar life histories. Mol Ecol. 16:3173–3186. PMid:17651195. http://dx.doi.org/10.1111/j.1365-294X.2007.03385.x

Bird CE, Karl SA, Smouse PE, Toonen RJ. 2011. Detecting and measuring genetic differentiation. *In:* Held C, Koenemann S, Schubart CD, editors. Phylogeography and population genetics in crustacea. CRC Press. p. 400. http://dx.doi.org/10.1201/b11113-4

Bourjea J, Lapegue S, Gagnevin L, Broderick D, Mortimer JA, Ciccione S, Roos D, Taquet C, Grizel H. 2007. Phylogeography of the green turtle, *Chelonia mydas,* in the southwest Indian Ocean. Mol Ecol. 16(1):175-186. PMid:17181729. http://dx.doi.org/10.1111/j.1365-294X.2006.03122.x

Bowen BW, Bass AL, Rocha LA, Grant WS, Robertson DR. 2001. Phylogeography of the trumpetfishes (*Aulostomus*): ring species complex on a global scale. Evolution. 55(5):1029–1039. http://dx.doi.org/10.1554/0014-3820(2001)055[1029:POTTAR]2.0.CO;2

Bowen BW, Rocha LA, Toonen RJ, Karl SA, Craig MT, DiBattista JD, Eble JA, Gaither MR, Skillings D, Bird CJ. 2013. The origins of tropical marine biodiversity. Trends Ecol Evol. 28(6):359–366. PMid:23453048. http://dx.doi.org/10.1016/j.tree.2013.01.018

Bowen BW, Shanker K, Yasuda N, Malay MCD, von der Heyden S, Paulay G, Rocha LA, Selkoe KA, Barber PH, Williams ST, et al. 2014. Phylogeography unplugged: comparative geographic surveys in the genomic era. Bull Mar Sci. 90:13–46. http://dx.doi.org/10.5343/bms.2013.1007

Bradbury IR, Bentzen P. 2007. Non-linear genetic isolation by distance: implications for dispersal estimation in anadromous and marine fish populations. Mar Ecol Prog Ser. 340:245–257. http://dx.doi.org/10.3354/meps340245

Briggs JC. 1974. Marine zoogeography. New York: McGraw-Hill.

Briggs JC. 1999. Coincident biogeographic patterns: Indo-West Pacific Ocean. Evolution. 53(2):326–335. http://dx.doi.org/10.2307/2640770

Carpenter KE, Barber PH, Crandall ED, Manjaji-Matsumoto BM, Juinio-Meñez MA, Santos MD, Starger CJ, Toha AHA. 2011. Comparative phylogeography of the Coral Triangle and implications for marine management. J Mar Biol. 2011:Article ID 396982, 14 p.

Carpenter KE, Springer VG. 2005. The center of the center of marine shore fish biodiversity: the Philippine Islands. Environ Biol Fish. 72(4):467–480. http://dx.doi.org/10.1007/s10641-004-3154-4

Chenoweth SF, Hughes JM. 2003. Oceanic interchange and nonequilibrium population structure in the estuarine dependent Indo-Pacific tasselfish, *Polynemus sheridani*. Mol Ecol. 12(9):2387-2397. PMid:12919476. http://dx.doi.org/10.1046/j.1365-294X.2003.01921.x

Chenoweth SF, Hughes JM, Keenan CP, Lavery S. 1998. Concordance between dispersal and mitochondrial gene flow: isolation by distance in a tropical teleost, *Lates calcarifer* (Australian barramundi). Heredity. 80:187–197. http://dx.doi.org/10.1046/j.1365-2540.1998.00292.x

Choat JH, Klanten OS, Van Herwerden L, Robertson DR, Clements KD. 2012. Patterns and processes in the evolutionary history of parrotfishes (Family Labridae). Biol J Linnean Soc. 107(3):529–557. http://dx.doi.org/10.1111/j.1095-8312.2012.01959.x

Concepcion GT, Kahng SE, Crepeau MW, Franklin EC, Coles SL, Toonen RJ. 2010. Resolving natural ranges and marine invasions in a globally distributed octocoral (genus *Carijoa*). Mar Ecol Prog Ser. 401:113–127. http://dx.doi.org/10.3354/meps08364

Connolly SR, Bellwood DR, Hughes TP. 2003. Indo-Pacific biodiversity of coral reefs: deviations from a mid-domain model. Ecology. 84(8):2178–2190. http://dx.doi.org/10.1890/02-0254

Craig MT, Eble JA, Bowen BW, Robertson DR. 2007. High genetic connectivity across the Indian and Pacific oceans in the reef fish *Myripristis berndti* (Holocentridae). Mar Ecol Prog Ser. 334:245–254. http://dx.doi.org/10.3354/meps334245

Crandall ED, Frey MA, Grosberg RK, Barber PH. 2008a. Contrasting demographic history and phylogeographical patterns in two Indo-Pacific gastropods. Mol Ecol. 17(2):611–626. PMid:18179436. http://dx.doi.org/10.1111/j.1365-294X.2007.03600.x

Crandall ED, Jones ME, Muñoz MM, Akinronbi B, Erdmann MV, Barber PH. 2008b. Comparative phylogeography of two seastars and their ectosymbionts within the Coral Triangle. Mol Ecol. 17(24):5276–5290. PMid:19067797. http://dx.doi.org/10.1111/j.1365-294X.2008.03995.x

Crandall ED, Treml EA, Barber PH. 2012. Coalescent and biophysical models of long-distance dispersal dynamics in Neritid snails. Mol Ecol. 21(22):5579–5598. PMid:23050562. http://dx.doi.org/10.1111/mec.12031

Daly-Engel TS, Randall JE, Bowen BW. 2012. Is the great barracuda (*Sphyraena barracuda*) a reef fish or a pelagic fish? The phylogeographic perspective. Mar Biol. 159(5):975–985. http://dx.doi.org/10.1007/s00227-012-1878-9

Dawson MN. 2012. Parallel phylogeographic structure in ecologically similar sympatric sister taxa. Mol Ecol. 21(4):987–1004. PMid:22229665. http://dx.doi.org/10.1111/j.1365-294X.2011.05417.x

DeBoer TS, Subia MD, Ambariyanto, Erdmann MV, Kovitvongsa K, Barber PH. 2008. Phylogeography and limited genetic connectivity in the endangered boring giant clam across the Coral Triangle. Conserv Biol. 22(5):1255–1266. PMid:18637905. http://dx.doi.org/10.1111/j.1523-1739.2008.00983.x

de Croos M, Palsson S. 2010. Mitochondrial DNA variation and population genetic structure of white shrimp *Fenneropenaeus indicus* along the coastal belt of Sri Lanka. Aquat Living Resour. 23(3):315–323. http://dx.doi.org/10.1051/alr/2010027

Dethmers KEM, Broderick D, Moritz C, Fitzsimmons NN, Limpus CJ, Lavery S, Whiting S, Guinea M, Prince RIT, Kennett R. 2006. The genetic structure of Australasian green turtles (*Chelonia mydas*): exploring the geographical scale of genetic exchange. Mol Ecol. 15(13):3931–3946. PMid:17054494. http://dx.doi.org/10.1111/j.1365-294X.2006.03070.x

DiBattista JD, Waldrop E, Bowen BW, Schultz JK, Gaither MR, Pyle RL, Rocha LA. 2012. Twisted sister species of pygmy angelfishes: discordance between taxonomy, coloration, and phylogenetics. Coral Reefs. 31:839–851. http://dx.doi.org/10.1007/s00338-012-0907-y

DiBattista JD, Wilcox C, Craig MT, Rocha LA, Bowen BW. 2011. Phylogeography of the Pacific blueline surgeonfish, *Acanthurus nigroris,* reveals high genetic connectivity and a cryptic endemic species in the Hawaiian Archipelago. J Mar Biol. 2011:1–17. http://dx.doi.org/10.1155/2011/839134

Doherty PJ, Planes S, Mather P. 1995. Gene flow and larval duration in seven species of fish from the Great Barrier Reef. Ecology. 76(8):2373–2391. http://dx.doi.org/10.2307/2265814

Drew J, Allen GR, Kaufman L, Barber PH. 2008. Endemism and regional color and genetic differences in five putatively cosmopolitan reef fishes. Conserv Biol. 22(4):965–975. PMid:18786099. http://dx.doi.org/10.1111/j.1523-1739.2008.01011.x

Duda TF, Lee T. 2009. Isolation and population divergence of a widespread Indo-west Pacific marine gastropod at Easter Island. Mar Biol. 156(6):1193-1202. http://dx.doi.org/10.1007/s00227-009-1161-x

Duda TF, Lessios HA. 2009. Connectivity of populations within and between major biogeographic regions of the tropical Pacific in *Conus ebraeus,* a widespread marine gastropod. Coral Reefs. 28(3):651–659. http://dx.doi.org/10.1007/s00338-009-0485-9

Duda TF, Palumbi SR. 1999. Population structure of the black tiger prawn, *Penaeus monodon,* among western Indian Ocean and western Pacific populations. Mar Biol. 134(4):705–710. http://dx.doi.org/10.1007/s002270050586

Duda TF, Terbio M, Chen G, Phillips S, Olenzek AM, Chang D, Morris DW. 2012. Patterns of population structure and historical demography of *Conus* species in the tropical Pacific. Am Malacological Bull. 30(1):175–187. http://dx.doi.org/10.4003/006.030.0116

Dudgeon CL, Broderick D, Ovenden JR. 2009. IUCN classification zones concord with, but underestimate, the population genetic structure of the zebra shark *Stegostoma fasciatum* in the Indo-West Pacific. Mol Ecol. 18(2):248–261. PMid:19192179. http://dx.doi.org/10.1111/j.1365-294X.2008.04025.x

Dudgeon CL, Gust N, Blair D. 2000. No apparent genetic basis to demographic differences in scarid fishes across continental shelf of the Great Barrier Reef. Mar Biol. 137(5–6):1059–1066. http://dx.doi.org/10.1007/s002270000403

Eble JA, Rocha LA, Craig MT, Bowen BW. 2011a. Not all larvae stay close to home: insights into marine population connectivity with a focus on the brown surgeonfish (*Acanthurus nigrofuscus*). J Mar Biol. 2011:1–12. http://dx.doi.org/10.1155/2011/518516

Eble JA, Toonen RJ, Sorenson L, Basch LV, Papastamatiou YP, Bowen BW. 2011b. Escaping paradise: larval export from Hawaii in an Indo-Pacific reef fish, the yellow tang *Zebrasoma flavescens*. Mar Ecol Prog Ser. 428:245–258. http://dx.doi.org/10.3354/meps09083

Ekman S. 1935. Tiergeographie des meeres. Leipzig: Akademische Verlagsgesellschaft MBH.

Ekman S. 1953. Zoogeography of the sea. London: Sidgwick and Jackson.

Eschmeyer WN, Fricke R, Fong JD, Polack DA. 2010. Marine fish diversity: history of knowledge and discovery (Pisces). Zootaxa. 2525:19–50.

Fauvelot C, Planes S. 2002. Understanding origins of present-day genetic structure in marine fish: biologically or historically driven patterns? Mar Biol. 141(4):773–788. http://dx.doi.org/10.1007/s00227-002-0869-7

Fernandez-Silva I, Whitney J, Wainwright B, Andrews KR, Toonen RJ, Ylitalo-Ward H, Bowen BW, Goetze E, Karl SA. 2013. Microsatellites for next-generation ecologists: a post-sequencing bioinformatics pipeline. PLoS One. 8(2):e55990. PMid:23424642. PMCid:PMC3570555. http://dx.doi.org/10.1371/journal.pone.0055990

Fitzpatrick JM, Carlon DB, Lippe C, Robertson DR. 2011. The west Pacific diversity hotspot as a source or sink for new species? Population genetic insights from the Indo-Pacific parrotfish *Scarus rubroviolaceus*. Mol Ecol. 20(2):219–234. PMid:21143329. http://dx.doi.org/10.1111/j.1365-294X.2010.04942.x

Forbes E. 1856. Map of the distribution of marine life. *In:* Johnston AK, editors. The physical atlas of natural phenomena (new edition). London: W Johnston and AK Johnston. p. 31.

Forsman Z, Barshis D, Hunter C, Toonen R. 2009. Shape-shifting corals: molecular markers show morphology is evolutionarily plastic in *Porites*. BMC Evol Biol. 9(1):45. PMid:19239678. PMCid:PMC2656472. http://dx.doi.org/10.1186/1471-2148-9-45

Fratini S, Ragionieri L, Cannicci S. 2010. Stock structure and demographic history of the Indo-West Pacific mud crab *Scylla serrata*. Estuar Coast Shelf Sci. 86(1):51–61. http://dx.doi.org/10.1016/j.ecss.2009.10.009

Fratini S, Vannini M. 2002. Genetic differentiation in the mud crab *Scylla serrata* (Decapoda: Portunidae) within the Indian Ocean. J Exp Mar Biol Ecol. 272(1):103–116. http://dx.doi.org/10.1016/S0022-0981(02)00052-7

Frey MA, Vermeij GJ. 2008. Molecular phylogenies and historical biogeography of a circumtropical group of gastropods (Genus: *Nerita*): implications for regional diversity patterns in the marine tropics. Mol Phylogenet Evol. 48(3):1067–1086. PMid:18586528. http://dx.doi.org/10.1016/j.ympev.2008.05.009

Fu YX. 1997. Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. Genetics. 147(2):915–925. PMid:9335623. PMCid:PMC1208208.

Gaither MR, Bowen BW, Bordenave TR, Rocha LA, Newman SJ, Gomez JA, van Herwerden L, Craig MT. 2011a. Phylogeography of the reef fish *Cephalopholis argus* (Epinephelidae) indicates Pleistocene isolation across the Indo-Pacific barrier with contemporary overlap in the Coral Triangle. BMC Evol Biol. 11:189. PMid:21722383. PMCid:PMC3145601. http://dx.doi.org/10.1186/1471-2148-11-189

Gaither MR, Jones SA, Kelley C, Newman SJ, Sorenson L, Bowen BW. 2011b. High connectivity in the deepwater snapper *Pristipomoides filamentosus* (Lutjanidae) across the Indo-Pacific with Isolation of the Hawaiian Archipelago. PLoS One. 6(12):e28913. PMid:22216141. PMCid:PMC3245230. http://dx.doi.org/10.1371/journal.pone.0028913

Gaither MR, Toonen RJ, Robertson DR, Planes S, Bowen BW. 2010. Genetic evaluation of marine biogeographical barriers: perspectives from two widespread Indo-Pacific snappers (*Lutjanus kasmira* and *Lutjanus fulvus*). J Biogeogr. 37(1):133–147. http://dx.doi.org/10.1111/j.1365-2699.2009.02188.x

Gopurenko D, Hughes JM. 2002. Regional patterns of genetic structure among Australian populations of the mud crab, *Scylla serrata* (Crustacea: Decapoda): evidence from mitochondrial DNA. Mar Freshwat Res. 53(5):849–857. http://dx.doi.org/10.1071/MF01225

Gopurenko D, Hughes JM, Keenan CP. 1999. Mitochondrial DNA evidence for rapid colonisation of the Indo-West Pacific by the mudcrab *Scylla serrata*. Mar Biol. 134:227–233. http://dx.doi.org/10.1007/s002270050541

Haig JA, Connolly RM, Hughes JM. 2010. Little shrimp left on the shelf: the roles that sea-level change, ocean currents and continental shelf width play in the genetic connectivity of a seagrass-associated species. J Biogeogr. 37(8):1570–1583.

Han ZQ, Li YZ, Chen GB, Gao TX. 2008. Population genetic structure of coral reef species *Plectorhinchus flavomaculatus* in South China Sea. Afr J Biotechnol. 7(11):1774–1781.

Hare M. 2001. Prospects for nuclear gene phylogeography. Trends Ecol Evol. 16:700–706. http://dx.doi.org/10.1016/S0169-5347(01)02326-6

Harrison HB, Williamson DH, Evans RD, Almany GR, Thorrold SR, Russ GR, Feldheim KA, Van Herwerden L, Planes S, Srinivasan M. 2012. Larval export from marine reserves and the recruitment benefit for fish and fisheries. Curr Biol. 22(11):1023–1028. PMid:22633811. http://dx.doi.org/10.1016/j.cub.2012.04.008

Hedrick PW. 2005. A standardized genetic differentiation measure. Evolution. 59(8):1633–1638. PMid:16329237.

Hellberg ME. 2006. No variation and low synonymous substitution rates in coral mtDNA despite high nuclear variation. BMC Evol Biol. 6(1):24. PMid:16542456. PMCid:PMC1431588. http://dx.doi.org/10.1186/1471-2148-6-24

Hickerson MJ, Meyer CP. 2008. Testing comparative phylogeographic models of marine vicariance and dispersal using a hierarchical Bayesian approach. BMC Evol Biol. 8(1):322. PMid:19038027. PMCid:PMC2614435. http://dx.doi.org/10.1186/1471-2148-8-322

Hoareau TB, Boissin E, Berrebi P. 2012. Evolutionary history of a widespread Indo-Pacific goby: the role of Pleistocene sea-level changes on demographic contraction/expansion dynamics. Mol Phylogenet Evol. 62(1):566–572. PMid:22037473. http://dx.doi.org/10.1016/j.ympev.2011.10.004

Hoeksema B. 2007. Delineation of the Indo-Malayan centre of maximum marine biodiversity: the Coral Triangle. Biogeogr Time Place: Distributions Barriers Islands. 29:117–178. http://dx.doi.org/10.1007/978-1-4020-6374-9_5

Hoffman EA, Kolm N, Berglund A, Arguello JR, Jones AG. 2005. Genetic structure in the coral-reef-associated Banggai cardinalfish, *Pterapogon kauderni*. Mol Ecol. 14(5):1367–1375. PMid:15813777. http://dx.doi.org/10.1111/j.1365-294X.2005.02538.x

Horne JB, Momigliano P, Welch DJ, Newman SJ, van Herwerden L. 2011. Limited ecological population connectivity suggests low demands on self-recruitment in a tropical inshore marine fish (*Eleutheronema tetradactylum:* Polynemidae). Mol Ecol. 20(11):2291–2306. PMid:21518062. http://dx.doi.org/10.1111/j.1365-294X.2011.05097.x

Horne JB, van Herwerden L, Choat JH, Robertson DR. 2008. High population connectivity across the Indo-Pacific: congruent lack of phylogeographic structure in three reef fish congeners. Mol Phylogenet Evol. 49(2):629–638. PMid:18804542. http://dx.doi.org/10.1016/j.ympev.2008.08.023

Huelsken T, Schreiber S, Hollmann M. 2011. COI amplification success from mucus-rich marine gastropods (Gastropoda: Naticidae) depends on DNA extraction method and preserving agent. Mitteilungen der Deutschen Malakozoologischen Gesellschaft. 85:17–26.

Imron JB, Hale P, Degnan BM, Degnan SM. 2007. Pleistocene isolation and recent gene flow in *Haliotis asinina,* an Indo-Pacific vetigastropod with limited dispersal capacity. Mol. Ecol. 16(2):289–304. PMid:17217345.

Iwamoto K, Takemura A, Yoshino T, Imai H. 2009. Molecular ecological study of *Siganus spinus* and *S. guttatus* from Okinawan waters based on mitochondrial DNA control region sequences. J. Oceanogr. 65(1):103–112. http://dx.doi.org/10.1007/s10872-009-0010-3

Johnson MS, Watts RJ, Black R. 1994. High levels of genetic subdivision on peripherally isolated populations of the atherinid fish *Craterocephalus capreoli* in the Houtman-Abrolhos Islands, Western Australia. Mar Biol. 119(2):179–184. http://dx.doi.org/10.1007/BF00349554

Karl SA, Avise JC. 1993. PCR-based assays of Mendelian polymorphisms from anonymous single-copy nuclear DNA: techniques and applications for population genetics. Mol Biol Evol. 10:342–361. PMid:8098128.

Klanten OS, Choat JH, van Herwerden L. 2007. Extreme genetic diversity and temporal rather than spatial partitioning in a widely distributed coral reef fish. Mar Biol. 150(4):659–670. http://dx.doi.org/10.1007/s00227-006-0372-7

Knittweis L, Kraemer WE, Timm J, Kochzius M. 2009. Genetic structure of *Heliofungia actiniformis* (Scleractinia: Fungiidae) populations in the Indo-Malay Archipelago: implications for live coral trade management efforts. Conserv Genet. 10(1):241–249. http://dx.doi.org/10.1007/s10592-008-9566-5

Knowlton N. 2000. Molecular genetic analyses of species boundaries in the sea. Hydrobiologia. 420(1):73–90. http://dx.doi.org/10.1023/A:1003933603879

Kochzius M, Nuryanto A. 2008. Strong genetic population structure in the boring giant clam, *Tridacna crocea,* across the Indo-Malay Archipelago: implications related to evolutionary processes and connectivity. Mol Ecol. 17:3775–3787. PMid:18662232. http://dx.doi.org/10.1111/j.1365-294X.2008.03803.x

Kochzius M, Seidel C, Hauschild J, Kirchhoff S, Mester P, Meyer-Wachsmuth I, Nuryanto A, Timm J. 2009. Genetic population structures of the blue starfish *Linckia laevigata* and its gastropod ectoparasite *Thyca crystallina*. Mar Ecol Prog Ser. 396:211–219. http://dx.doi.org/10.3354/meps08281

Kon T, Nohara M, Nishida M, Sterrer W, Nishikawa T. 2006. Hidden ancient diversification in the circumtropical lancelet *Asymmetron lucayanum* complex. Mar Biol. 149(4):875–883. http://dx.doi.org/10.1007/s00227-006-0271-y

Lacson JM, Clark S. 1995. Genetic divergance of Maldivian and Micronesian demes of the damselfishes *Stegastes nigricans, Chriysiptera biocellata, C. glauca* and *C. leucopoma* (Pomacentridae). Mar Biol. 121(4):585–590. http://dx.doi.org/10.1007/BF00349293

Ladd HS. 1960. Origin of the Pacific island molluscan fauna. Am J Sci. 258A:137–150.

Lavery S, Moritz C, Fielder DR. 1995. Changing patterns of population structure and gene flow at different spatial scales in *Birgus latro* (the coconut crab) Heredity. 74:531–541. http://dx.doi.org/10.1038/hdy.1995.75

Lessios HA, Robertson DR. 2006. Crossing the impassable: genetic connections in 20 reef fishes across the eastern Pacific barrier. Proc Roy Soc B: Biol Sci. 273(1598):2201. PMid:16901840. PMCid:PMC1635520. http://dx.doi.org/10.1098/rspb.2006.3543

Lin TY, Liu LL. 2008. Low levels of genetic differentiation among populations of the coral-inhabiting snail *Coralliophila violacea* (Gastropoda: Coralliophilidae) in regions of the Kuroshio and South China Sea. Zool Stud. 47(1):17–24.

Lind CE, Evans BS, Taylor JJU, Jerry DR. 2007. Population genetics of a marine bivalve, *Pinctada maxima,* throughout the Indo-Australian Archipelago shows differentiation and decreased diversity at range limits. Mol Ecol. 16(24):5193–5203. PMid:18028303. http://dx.doi.org/10.1111/j.1365-294X.2007.03598.x

Liu S-YV, Kokita T, Dai C-F. 2008. Population genetic structure of the neon damselfish (*Pomacentrus coelestis*) in the northwestern Pacific Ocean. Mar Biol. 154(4):745–753. http://dx.doi.org/10.1007/s00227-008-0967-2

Liu Q, Li SJ, Li Z, Wang G. 2007. Species composition in genus *Scylla* from the coast of southeast China. J Fish China. 31:211–219.

Lord C, Lorion J, Dettai A, Watanabe S, Tsukamoto K, Cruaud C, Keith P. 2012. From endemism to widespread distribution: phylogeography of three amphidromous *Sicyopterus species* (Teleostei: Gobioidei: Sicydiinae). Mar Ecol Prog Ser. 455:269–285. http://dx.doi.org/10.3354/meps09617

Ludt WB, Bernal MA, Bowen BW, Rocha LA. 2012. Living in the past: phylogeography and population histories of Indo-Pacific wrasses (genus *Halichoeres*) in shallow lagoons versus outer reef slopes. PLoS One. 7(6):e38042. PMid:22701597. PMCid:PMC3368945. http://dx.doi.org/10.1371/journal.pone.0038042

Lukoschek V, Waycott M, Keogh JS. 2008. Relative information content of polymorphic microsatellites and mitochondrial DNA for inferring dispersal and population genetic structure in the olive sea snake, *Aipysurus laevis.* Mol Ecol. 17(13):3062–3077. PMid:18494766. http://dx.doi.org/10.1111/j.1365-294X.2008.03815.x

Lukoschek V, Waycott M, Marsh H. 2007. Phylogeography of the olive sea snake, *Aipysurus laevis* (Hydrophiinae) indicates Pleistocene range expansion around northern Australia but low contemporary gene flow. Mol Ecol. 16(16):3406–3422. PMid:17688542. http://dx.doi.org/10.1111/j.1365-294X.2007.03392.x

Macaranas JM, Ablan CA, Pante MJR, Benzie JAH, Williams ST. 1992. Genetic structure of giant clam (*Tridacna derasa*) populations from reefs in the Indo-Pacific. Mar Biol. 113(2):231–238.

Magsino RM, Juinio-Meñez MA. 2008. The influence of contrasting life history traits and oceanic processes on genetic structuring of rabbitfish populations *Siganus argenteus* and *Siganus fuscescens* along the eastern Philippine coasts. Mar Biol. 154(3):519–532. http://dx.doi.org/10.1007/s00227-008-0946-7

Mahidol C, Na-Nakorn U, Sukmanomon S, Taniguchi N, Nguyen TTT. 2007. Mitochondrial DNA diversity of the Asian moon scallop, *Amusium pleuronectes* (Pectinidae), in Thailand. Mar Biotechnol. 9(3):352–359. PMid:17549563. http://dx.doi.org/10.1007/s10126-006-6137-y

Mandal A, Rao D, Karuppaiah D, Gopalakrishnan A, Pozhoth J, Samraj YCT, Doyle RW. 2012. Population genetic structure of *Penaeus monodon,* in relation to monsoon current patterns in southwest, east and Andaman coastal waters of India. Gene. 491(2):149–157. PMid:22020227. http://dx.doi.org/10.1016/j.gene.2011.10.002

Meyer CP. 2003. Molecular systematics of cowries (Gastropoda: Cypraeidae) and diversification patterns in the tropics. Biol J Linnean Soc. 79(3):401–459. http://dx.doi.org/10.1046/j.1095-8312.2003.00197.x

Meyer CP, Geller JB, Paulay G. 2005. Fine scale endemism on coral reefs: archipelagic differentiation in turbinid gastropods. Evolution. 59(1):113–125. PMid:15792232.

Miller-Sims VC, Gerlach G, Kingsford MJ, Atema J. 2008. Dispersal in the spiny damselfish, *Acanthochromis polyacanthus*, a coral reef fish species without a larval pelagic stage. Mol Ecol. 17(23):5036–5048. PMid:19120989. http://dx.doi.org/10.1111/j.1365-294X.2008.03986.x

Mirams AGK, Treml EA, Shields JL, Liggins L, Riginos C. 2011. Vicariance and dispersal across an intermittent barrier: population genetic structure of marine animals across the Torres Strait land bridge. Coral Reefs. 30(4):937–949. http://dx.doi.org/10.1007/s00338-011-0767-x

Moritz C. 1994. Applications of mitochondrial DNA analysis in conservation: a critical review. Mol Ecol. 3(4):401–411. http://dx.doi.org/10.1111/j.1365-294X.1994.tb00080.x

Moritz C, Faith DP. 2002. Comparative phylogeography and the identification of genetically divergent areas for conservation. Mol Ecol. 7(4):419–429. http://dx.doi.org/10.1046/j.1365-294x.1998.00317.x

Muths D, Tessier E, Gouws G, Craig M, Mwale M, Mwaluma J, Mwandya A, Bourjea J. 2011. Restricted dispersal of the reef fish *Myripristis berndti* at the scale of the SW Indian Ocean. Mar Ecol Prog Ser. 443:167–180. http://dx.doi.org/10.3354/meps09394

Nuryanto A, Kochzius M. 2009. Highly restricted gene flow and deep evolutionary lineages in the giant clam *Tridacna maxima*. Coral Reefs. 28(3):607-619. http://dx.doi.org/10.1007/s00338-009-0483-y

Oksanen J, Guillaume Blanchet F, Kindt R, Legendre P, Minchin PR, O'Hara RB, Simpson GL, Solymos P, Henry M, Stevens H, et al. 2012. Vegan: community ecology package. R package version 2.0-4.

Otwoma LM. 2012. Genetic population structure of the coral reef starfish *Linckia laevigata* in the Indo-West Pacific. MS thesis. Free University of Brussels. p. 73.

Ovenden JR, Lloyd J, Newman SJ, Keenan CP, Slater LS. 2002. Spatial genetic subdivision between northern Australian and southeast Asian populations of *Pristipomoides multidens:* a tropical marine reef fish species. Fish Res. 59(1–2):57–69. http://dx.doi.org/10.1016/S0165-7836(01)00415-5

Ovenden JR, Salini J, O'Connor S, Street R. 2004. Pronounced genetic population structure in a potentially vagile fish species (*Pristipomoides multidens,* Teleostei: Perciformes: Lutjanidae) from the East Indies triangle. Mol Ecol. 13(7):1991–1999. PMid:15189219. http://dx.doi.org/10.1111/j.1365-294X.2004.02210.x

Palumbi SR. 1994. Genetic divergence, reproductive isolation, and marine speciation. Ann Rev Ecol Syst. 25:547–572. http://dx.doi.org/10.1146/annurev.es.25.110194.002555

Palumbi SR. 1997. Molecular biogeography of the Pacific. Coral Reefs. 16:S47–S52. http://dx.doi.org/10.1007/s003380050241

Palumbi SR, Grabowsky G, Duda T, Geyer L, Tachino N. 1997. Speciation and population genetic structure in tropical Pacific sea urchins. Evolution. 51(5):1506–1517. http://dx.doi.org/10.2307/2411203

Paulay G, Meyer C. 2006. Dispersal and divergence across the greatest ocean region: Do larvae matter? Integrative Comp Biol. 46(3):269–281. PMid:21672741. http://dx.doi.org/10.1093/icb/icj027

Plaisance L, Rousset V, Morand S, Littlewood DTJ. 2008. Colonization of Pacific islands by parasites of low dispersal ability: phylogeography of two monogenean species parasitizing butterflyfishes in the South Pacific Ocean. J Biogeogr. 35(1):76–87.

Planes S, Fauvelot C. 2002. Isolation by distance and vicariance drive genetic structure of a coral reef fish in the Pacific Ocean. Evolution. 56(2):378–399. PMid:11926506.

Prakoon W, Tunkijjanukij S, Nguyen TTT, Na-Nakorn U. 2010. Spatial and temporal genetic variation of green mussel, *Perna viridis* in the Gulf of Thailand and implication for aquaculture. Mar Biotechnol. 12(5):506–515. PMid:19941027. http://dx.doi.org/10.1007/s10126-009-9234-x

Puritz JB, Addison JA, Toonen RJ. 2012. Next-generation phylogeography: a targeted approach for multilocus sequencing of non-model organisms. PloS One. 7(3):e34241. PMid:22470543. PMCid:PMC3314618. http://dx.doi.org/10.1371/journal.pone.0034241

R Core Team. 2012. R: a language and environment for statistical computing. 2.15.1 ed. Vienna, Austria: R Foundation for Statistical Computing.

Ramon ML, Nelson PA, Martini E, Walsh WJ, Bernardi G. 2008. Phylogeography, historical demography, and the role of post-settlement ecology in two Hawaiian damselfish species. Mar Biol. 153(6):1207–1217. http://dx.doi.org/10.1007/s00227-007-0894-7

Ravago-Gotanco RG, Juinio-Menez MA. 2010. Phylogeography of the mottled spinefoot *Siganus fuscescens:* Pleistocene divergence and limited genetic connectivity across the Philippine archipelago. Mol Ecol. 19(20):4520–4534. PMid:20875063. http://dx.doi.org/10.1111/j.1365-294X.2010.04803.x

Reaka ML, Rodgers PJ, Kudla AU. 2008. Patterns of biodiversity and endemism on Indo-West Pacific coral reefs. Proc Natl Acad Sci USA. 105:11474–11481. PMid:18695226. PMCid:PMC2556415. http://dx.doi.org/10.1073/pnas.0802594105

Renema W, Bellwood D, Braga J, Bromfield K, Hall R, Johnson K, Lunt P, Meyer C, McMonagle L, Morley R. 2008. Hopping hotspots: global shifts in marine biodiversity. Science. 321(5889):654–657. PMid:18669854. http://dx.doi.org/10.1126/science.1155674

Rhodes KL, Lewis RI, Chapman RW, Sadovy Y. 2003. Genetic structure of camouflage grouper, *Epinephelus polyphekadion* (Pisces: Serranidae), in the western central Pacific. Mar Biol. 142(4):771–776.

Riginos C, Douglas KE, Jin Y, Shanahan DF, Treml EA. 2011. Effects of geography and life history traits on genetic differentiation in benthic marine fishes. Ecography. 34(4):566–575. http://dx.doi.org/10.1111/j.1600-0587.2010.06511.x

Roberts CM, McClean CJ, Veron JEN, Hawkins JP, Allen GR, McAllister DE, Mittermeier CG, Schueler FW, Spalding M, Wells F. 2002. Marine biodiversity hotspots and conservation priorities for tropical reefs. Science. 295(5558):1280. PMid:11847338. http://dx.doi.org/10.1126/science.1067728

Rocha L, Craig M, Bowen B. 2007. Phylogeography and the conservation of coral reef fishes. Coral Reefs. 26(3):501–512. http://dx.doi.org/10.1007/s00338-007-0261-7

Schultz JK, Feldheim KA, Gruber SH, Ashley MV, McGovern TM, Bowen BW. 2008. Global phylogeography and seascape genetics of the lemon sharks (genus *Negaprion*). Mol Ecol. 17(24):5336–5348. PMid:19121001. http://dx.doi.org/10.1111/j.1365-294X.2008.04000.x

Selkoe K, Toonen RJ. 2011. Marine connectivity: a new look at pelagic larval duration and genetic metrics of dispersal. Mar Ecol Prog Ser. 436:291–305. http://dx.doi.org/10.3354/meps09238

Selkoe KA, Watson J, White C, Ben-Horin T, Iacchei M, Miterai S, Siegel D, Gaines SD, Toonen RJ. 2010. Taking the chaos out of genetic patchiness: seascape genetics reveals ecological and oceanographic drivers of genetic patterns in three temperate reef species. Mol Ecol. 19(17):3708–3726. PMid:20723063. http://dx.doi.org/10.1111/j.1365-294X.2010.04658.x

Shearer TL, Van Oppen MJ, Romano SL, Worheide G. 2002. Slow mitochondrial DNA sequence evolution in the Anthozoa (Cnidaria). Mol Ecol. 11:2475–2487. PMid:12453233. http://dx.doi.org/10.1046/j.1365-294X.2002.01652.x

Tajima F. 1989. Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. Genetics. 123:585–595. PMid:2513255. PMCid:PMC1203831.

Tenopir C, Allard S, Douglass KL, Aydinoglu AU, Wu L, Read E, Manoff M, Frame M. 2011. Data sharing by scientists: practices and perceptions. PloS One. 6(6):e21101. PMid:21738610. PMCid:PMC3126798. http://dx.doi.org/10.1371/journal.pone.0021101

Teske PR, Hamilton H, Palsboll PJ, Choo CK, Gabr H, Lourie SA, Santos M, Sreepada A, Cherry MI, Matthee CA. 2005. Molecular evidence for long-distance colonization in an Indo-Pacific seahorse lineage. Mar Ecol Prog Ser. 286:249–260. http://dx.doi.org/10.3354/meps286249

Thacker CE, Thompson AR, Roje DM, Shaw EY. 2008. New expansions in old clades: population genetics and phylogeny of *Gnatholepis* species (Teleostei: Gobioidei) in the Pacific. Mar Biol. 153(3):375–385. http://dx.doi.org/10.1007/s00227-007-0814-x

Timm J, Kochzius M. 2008. Geological history and oceanography of the Indo-Malay Archipelago shape the genetic population structure in the false clown anemonefish (*Amphiprion ocellaris*). Mol Ecol. 17(18):3999–4014. PMid:19238702. http://dx.doi.org/10.1111/j.1365-294X.2008.03881.x

Timm J, Planes S, Kochzius M. 2012. High similarity of genetic population structure in the false clown anemonefish (*Amphiprion ocellaris*) found in microsatellite and mitochondrial control region analysis. Conserv Genet. 13(3):693–706. http://dx.doi.org/10.1007/s10592-012-0318-1

Timmers MA, Andrews KR, Bird CE, deMaintenton MJ, Brainard RE, Toonen RJ. 2011. Widespread dispersal of the crown-of-thorns sea star, *Acanthaster planci*, across the Hawaiian Archipelago and Johnston Atoll. J Mar Biol. 2011:Article ID 934269, 10 p.

Timmers MA, Bird CE, Skillings DJ, Smouse PE, Toonen RJ. 2012. There's no place like home: crown-of-thorns outbreaks in the central Pacific are regionally derived and independent events. PLoS One. 7(2):e31159. PMid:22363570. PMCid:PMC3281911. http://dx.doi.org/10.1371/journal.pone.0031159

Tittensor DP, Mora C, Jetz W, Lotze HK, Ricard D, Berghe EV, Worm B. 2010. Global patterns and predictors of marine biodiversity across taxa. Nature. 466(7310):1098–1101. PMid:20668450. http://dx.doi.org/10.1038/nature09329

Toonen RJ. 1997. Microsatellites for ecologists: non-radioactive isolation and amplification protocols for microsatellite markers. Unpublished manuscript available from the author online: http://www.academia.edu/950049/Microsatellites_for_ecologists_non-radioactive_isolation_and_amplification_protocols_for_microsatellite_markers

Toonen RJ, Andrews KR, Baums IB, Bird CE, Concepcion GT, Daly-Engel TS, Eble JA, Faucci A, Gaither MR, Iacchei M. 2011. Defining boundaries for ecosystem-based management: a multispecies case study of marine connectivity across the Hawaiian Archipelago. J Mar Biol. 2011:Article ID 460173, 13 p.

Tsang LM, Chan BKK, Wu TH, Ng WC, Chatterjee T, Williams GA, Chu KH. 2008. Population differentiation in the barnacle *Chthamalus malayensis:* postglacial colonization and recent connectivity across the Pacific and Indian oceans. Mar Ecol Prog Ser. 364:107–118. http://dx.doi.org/10.3354/meps07476

Tsoi KH, Chan TY, Chu KH. 2007. Molecular population structure of the kuruma shrimp *Penaeus japonicus* species complex in western Pacific. Mar Biol. 150(6):1345–1364. http://dx.doi.org/10.1007/s00227-006-0426-x

Uehara T, Shingaki M. 1985. Taxonomic studies on the four types of sea urchin, *Echinometra mathaei* from Okinawa, Japan. Zoo Sci. 2:1009–1015.

Uthicke S, Benzie JAH. 2001. Restricted gene flow between *Holothuria scabra* (Echinodermata: Holothuroidea) populations along the north-east coast of Australia and the Solomon Islands. Mar Ecol Prog Ser. 216:109–117. http://dx.doi.org/10.3354/meps216109

Uthicke S, Benzie JAH. 2003. Gene flow and population history in high dispersal marine invertebrates: mitochondrial DNA analysis of *Holothuria nobilis* (Echinodermata: Holothuroidea) populations from the Indo-Pacific. Mol Ecol. 12(10):2635–2648. PMid:12969467. http://dx.doi.org/10.1046/j.1365-294X.2003.01954.x

Uthicke S, Benzie JAH, Ballment E. 1999. Population genetics of the fissiparous holothurian *Stichopus chloronotus* (Aspidochirotida) on the Great Barrier Reef, Australia. Coral Reefs. 18(2):123–132. http://dx.doi.org/10.1007/s003380050166

Uthicke S, Conand C, Benzie JAH. 2001. Population genetics of the fissiparous holothurians *Stichopus chloronotus* and *Holothuria atra* (Aspidochirotida): a comparison between the Torres Strait and La Reunion. Mar Biol. 139(2):257–265. http://dx.doi.org/10.1007/s002270100579

Uthicke S, Purcell S. 2004. Preservation of genetic diversity in restocking of the sea cucumber *Holothuria scabra* investigated by allozyme electrophoresis. Can J Fish Aquat Sci. 61(4):519–528. http://dx.doi.org/10.1139/f04-013

Vagelli A, Burford M, Bernardi G. 2008. Fine scale dispersal in Banggai Cardinalfish, *Pterapogon kaudemi,* a coral reef species lacking a pelagic larval phase. Mar Genom. 1(3–4):129–134. PMid:21798164. http://dx.doi.org/10.1016/j.margen.2009.01.001

Vagelli A, Burford M, Bernardi G. 2009. Fine scale dispersal in Banggai Cardinalfish, *Pterapogon kauderni,* a coral reef species lacking a pelagic larval phase. Mar Genom. 1:129–134. PMid:21798164. http://dx.doi.org/10.1016/j.margen.2009.01.001

van Herwerden L, Aspden WJ, Newman SJ, Pegg GG, Briskey L, Sinclair W. 2009a. A comparison of the population genetics of *Lethrinus miniatus* and *Lutjanus sebae* from the east and west coasts of Australia: evidence for panmixia and isolation. Fish Res. 100(2):148–155. http://dx.doi.org/10.1016/j.fishres.2009.07.003

van Herwerden L, Benzie J, Davies C. 2003. Microsatellite variation and population genetic structure of the red throat emperor on the Great Barrier Reef. J Fish Biol. 62(5):987–999. http://dx.doi.org/10.1046/j.1095-8649.2003.00075.x

van Herwerden L, Choat JH, Newman SJ, Leray M, Hillersoy G. 2009b. Complex patterns of population structure and recruitment of *Plectropomus leopardus* (Pisces: Epinephelidae) in the Indo-West Pacific: implications for fisheries management. Mar Biol. 156(8):1595–1607. http://dx.doi.org/10.1007/s00227-009-1195-0

Vargas S, Schuster A, Sacher K, Büttner G, Schätzle S, Läuchli B, Hall K, Hooper JNA, Erpenbeck D, Wörheide G. 2012. Barcoding sponges: an overview based on comprehensive sampling. PloS One. 7(7):e39345. PMid:22802937. PMCid:PMC3389008. http://dx.doi.org/10.1371/journal.pone.0039345

Veron JEN. 1995. Corals in space and time. The biogeography and evolution of the Scleractinia. Ithaca, London: Cornell University Press (Comstock).

Visram S, Yang M-C, Pillay RM, Said S, Henriksson O, Grahn M, Chen CA. 2010. Genetic connectivity and historical demography of the blue barred parrotfish (*Scarus ghobban*) in the western Indian Ocean. Mar Biol. 157(7):1475–1487. http://dx.doi.org/10.1007/s00227-010-1422-8

Vogler C, Benzie J, Lessios H, Barber P, Wörheide G. 2008. A threat to coral reefs multiplied? Four species of crown-of-thorns starfish. Biol Lett. 4(6):696–699. PMid:18832058. PMCid:PMC2614177. http://dx.doi.org/10.1098/rsbl.2008.0454

von der Heyden S, Beger M, Toonen R, Ravago-Gotanco R, Fauvelot C, Juinio-Meñez MA, Bird CE, Bernardi G. 2014. The application of genetics to marine management and conservation: examples from the Indo-Pacific. Bull Mar Sci. 90:123–158. http://dx.doi.org/10.5343/bms.2012.1079

Wares JP. 2009. Natural distributions of mitochondrial sequence diversity support new null hypotheses. Evolution. 64(4):1136–1142. PMid:19863588. http://dx.doi.org/10.1111/j.1558-5646.2009.00870.x

Weersing K, Toonen RJ. 2009. Population genetics, larval dispersal, and connectivity in marine systems. Mar Ecol Prog Ser. 393(1):12.

Wessel P, Smith WHF. 1996. A global, self-consistent, hierarchical, high-resolution shoreline database. J Geophys Res. 101(B4):8741–8743. http://dx.doi.org/10.1029/96JB00104

Whitlock MC. 2011. Data archiving in ecology and evolution: best practices. Trends Ecol Evol. 26(2):61–65. PMid:21159406. http://dx.doi.org/10.1016/j.tree.2010.11.006

Williams ST, Benzie JAH. 1993. Genetic consequences of long larval life in the starfish *Linckia laevigata* (Echinodermata, Asteroidea) on the Great Barrier Reef. Mar Biol. 117(1):71–77. http://dx.doi.org/10.1007/BF00346427

Williams ST, Benzie JAH. 1996. Genetic uniformity of widely separated populations of the coral reef starfish *Linckia laevigata* from the east Indian and west Pacific oceans, revealed by allozyme electrophoresis. Mar Biol. 126(1):99–107. http://dx.doi.org/10.1007/BF00571381

Winters KL, van Herwerden L, Choat JH, Robertson DR. 2010. Phylogeography of the Indo-Pacific parrotfish *Scarus psittacus:* isolation generates distinctive peripheral populations in two oceans. Mar Biol. 157(8):1679–1691. http://dx.doi.org/10.1007/s00227-010-1442-4

WoRMS Editorial Board. 2012. World Register of Marine Species. Available from: http://www.marinespecies.org. Accessed 15 December, 2012.

Xia JH, Huang JH, Gong JB, Jiang SG. 2008. Significant population genetic structure of yellowfin seabream *Acanthopagrus latus* in China. J Fish Biol. 73(8):1979–1992. http://dx.doi.org/10.1111/j.1095-8649.2008.02010.x

Yap CK, Chong CM, Tan SG. 2011. Allozyme polymorphisms in horseshoe crabs, *Carcinoscorpius rotundicauda,* collected from polluted and unpolluted intertidal areas in Peninsular Malaysia. Environ Monit Assess. 174(1–4):389–400. PMid:20437264. http://dx.doi.org/10.1007/s10661-010-1464-x

Yap CK, Tan SG, Ismail A, Omar H. 2004. Allozyme polymorphisms and heavy metal levels in the green-lipped mussel *Perna viridis* (Linnaeus) collected from contaminated and uncontaminated sites in Malaysia. Environ Int. 30(1):39–46. http://dx.doi.org/10.1016/S0160-4120(03)00144-2

Yasuda N, Nagai S, Hamaguchi M, Okaji K, Gerard K, Nadaoka K. 2009. Gene flow of *Acanthaster planci* (L.) in relation to ocean currents revealed by microsatellite analysis. Mol Ecol. 18(8):1574–1590. PMid:19302361. http://dx.doi.org/10.1111/j.1365-294X.2009.04133.x

Yue GH, Zhu ZY, Lo LC, Wang CM, Lin G, Fenf F, Pang HY, Li J, Gong P, Liu HM, et al. 2009. Genetic variation and population structure of Asian seabass (*Lates calcarifer*) in the Asia-Pacific region. Aquaculture. 293(1–2):22–28. http://dx.doi.org/10.1016/j.aquaculture.2009.03.053

Zhang JB, Cai ZP, Huang LM. 2006. Population genetic structure of crimson snapper *Lutjanus erythropterus* in East Asia, revealed by analysis of the mitochondrial control region. Ices J Mar Sci. 63(4):693–704. http://dx.doi.org/10.1016/j.icesjms.2006.01.00

Appendix 1. All species included in the dataset, with their citations and the genetic marker used in the study. Names in black are those species for which species authority was derived from the Integrated Taxonomic Information System, [#] represents those derived from the World Register of Marine Species and [♂] represents those derived from Fishbase.

Species name and authority	Citations for studies included in this data set	Marker
Acanthaster planci (Linnaeus, 1758)	Benzie 1999, Yasuda et al. 2009	Allozymes, Microsatellites
Acanthochromis polyacanthus (Bleeker, 1855)	Doherty et al. 1995, Miller-Sims et al. 2008	Allozymes, Microsatellites
Acanthopagrus latus (Houttuyn, 1782)	Xia et al. 2008	MtDNA
Acanthurus nigrofuscus (Forsskål, 1775)	Eble et al. 2011a	MtDNA
Acanthurus nigroris Valenciennes in Cuvier and Valenciennes, 1835	DiBattista et al. 2011	MtDNA
Acanthurus triostegus (Linnaeus, 1758)	Mirams et al. 2011, Planes and Fauvelot 2002	Allozymes, MtDNA
Aipysurus laevis Lacépède, 1804	Lukoschek et al. 2008, Lukoschek et al. 2007	Microsatellites, MtDNA
Amphiprion melanopus Bleeker, 1852	Doherty et al. 1995, Drew et al. 2008	Allozymes, MtDNA
Amphiprion ocellaris Cuvier in Cuvier and Valenciennes, 1830	Timm and Kochzius 2008, Timm et al. 2012	MtDNA, Microsatellites
Amusium pleuronectes (Linnaeus, 1758) [#]	Mahidol et al. 2007	MtDNA
Apogon doederleini Jordan and Snyder, 1901	Mirams et al. 2011	MtDNA
Asymmetron lucayanum Andrews, 1893	Kon et al. 2006	MtDNA
Aulostomus chinensis (Linnaeus, 1766)	Bowen et al. 2001	MtDNA
Birgus latro (Linnaeus, 1767)[#]	Lavery et al. 1995	Allozymes
Carcinoscorpius rotundicauda (Latreille, 1802)[#]	Yap et al. 2011	Allozymes
Carijoa riisei (Duchassaing and Michelotti, 1860)	Concepcion et al. 2010	MtDNA, other nuclear markers
Centropyge flavissima (Cuvier in Cuvier and Valenciennes, 1831)	DiBattista et al. 2012	MtDNA
Cephalopholis argus Bloch and Schneider, 1801	Gaither et al. 2011a	MtDNA, other nuclear markers
Chaetodon citrinellus Cuvier in Cuvier and Valenciennes, 1831	Fauvelot and Planes 2002	Allozymes
Chaetodon quadrimaculatus Gray, 1831	Fauvelot and Planes 2002	Allozymes
Chelonia mydas (Linnaeus, 1758)	Bourjea et al. 2007, Dethmers et al. 2006	MtDNA
Chlorurus sordidus (Forsskål, 1775)	Bay et al. 2004, Dudgeon et al. 2000	MtDNA
Chromis atripectoralis Welander and Schultz, 1951	Doherty et al. 1995	Allozymes
Chromis xanthura (Bleeker, 1854)	Fauvelot and Planes 2002	Allozymes
Chrysiptera glauca (Cuvier in Cuvier and Valenciennes, 1830)	Fauvelot and Planes 2002	Allozymes
Chrysiptera leucopoma (Cuvier in Cuvier and Valenciennes, 1830)	Lacson and Clark 1995	Allozymes

Appendix 1. Continued.

Species name and authority	Citations for studies included in this data set	Marker
Chrysiptera talboti (Allen, 1975)	Drew et al. 2008	MtDNA
Chthamalus malayensis Pilsbry, 1916[#]	Tsang et al. 2008	MtDNA
Clavularia koellikeri (Dean, 1927)[#]	Bastidas 2002	Allozymes
Conus chaldaeus (Röding, 1798)[#]	Duda et al. 2012	MtDNA
Conus ebraeus Linnaeus, 1758[#]	Duda and Lessios 2009	MtDNA
Conus miliaris Hwass in Bruguière, 1792[#]	Duda and Lee 2009	MtDNA
Conus sanguinolentus Quoy and Gaimard, 1834 [#]	Duda et al. 2012	MtDNA
Coralliophila violacea (Kiener, 1836)[#]	Lin and Liu 2008	Allozymes
Craterocephalus capreoli (Rendahl, 1922)	Johnson et al. 1994	Allozymes
Dascyllus albisella Gill, 1862	Ramon et al. 2008	MtDNA
Dascyllus aruanus (Linnaeus, 1758)	Fauvelot and Planes 2002	Allozymes
Dascyllus trimaculatus (Rüppell, 1829)	Mirams et al. 2011	MtDNA
Echinometra mathaei (Blainville, 1825)[#]	Palumbi et al. 1997	MtDNA
Echinometra oblonga (Blainville, 1825)[#]	Palumbi et al. 1997	MtDNA
Echinometra sp. C. first mentioned in Uehara and Shingaki 1985	Palumbi et al. 1997	MtDNA
Eleutheronema tetradactylum (Shaw, 1804)	Horne et al. 2011	MtDNA, Microsatellites
Epinephelus coioides (Hamilton, 1822)	Antoro et al. 2006	Microsatellites
Epinephelus polyphekadion (Bleeker, 1849)	Rhodes et al. 2003	Microsatellites
Euryhaliotrematoides grandis (Mizelle and Kritsky, 1969) [#] revised to *Euryhaliotrema grandis* Kritsky 2012	Plaisance et al. 2008	MtDNA
Fenneropenaeus indicus (H.Milne-Edwards, 1837)	de Croos and Palsson 2010	MtDNA
Forcipiger flavissimus Jordan and McGregor in Jordan and Evermann, 1898	Fauvelot and Planes 2002	Allozymes
Gnatholepis anjerensis (Bleeker, 1851)	Thacker et al. 2008	Microsatellites
Gnatholepis scapulostigma Herre, 1953[#] synonym of *G. cauerensis* (Bleeker, 1853)	Thacker et al. 2008	Microsatellites
Halichoeres claudia Randall & Rocha, 2009[#]	Ludt et al. 2012	MtDNA
Halichoeres ornatissimus (Garrett, 1863)	Ludt et al. 2012	MtDNA
Halichoeres trimaculatus (Quoy and Gaimard, 1834)	Ludt et al. 2012	MtDNA

Appendix 1. Continued.

Species name and authority	Citations for studies included in this data set	Marker
Haliotis asinina Linnaeus, 1758	Imron et al. 2007	MtDNA
Haptosquilla glyptocercus (Wood-Mason, 1875)#	Barber et al. 2002	MtDNA
Haptosquilla pulchella (Miers, 1880)#	Barber et al. 2002	MtDNA
Heliofungia actiniformis (Quoy and Gaimard, 1833)	Knittweis et al. 2009	Other Nuclear Markers
Hippocampus kuda Bleeker, 1852	Teske et al. 2005	MtDNA
Holothuria (Halodeima) atra Jaeger, 1833	Uthicke et al. 2001	Allozymes
Holothuria (Microthele) nobilis (Selenka, 1867)	Uthicke and Benzie 2003	MtDNA
Holothuria (Metriatyla) scabra Jaeger, 1833	Uthicke and Benzie 2001, Uthicke and Purcell 2004	Allozymes
Lates calcarifer (Bloch, 1790)	Chenoweth et al. 1998, Yue et al. 2009	MtDNA, Microsatellites
Lethrinus miniatus (Forster in Bloch and Schneider, 1801)	van Herwerden et al. 2009a, van Herwerden et al. 2003	Microsatellites, MtDNA
Linckia laevigata (Linnaeus, 1758)#	Crandall et al. 2008b, Kochzius et al. 2009, Williams and Benzie 1993, 1996	MtDNA, Allozymes
Lutjanus erythropterus Bloch, 1790	Zhang et al. 2006	MtDNA
Lutjanus fulvus (Forster in Bloch and Schneider, 1801)	Gaither et al. 2010	MtDNA
Lutjanus kasmira (Forsskål, 1775)	Gaither et al. 2010	MtDNA
Lutjanus sebae (Cuvier, 1816)	van Herwerden et al. 2009a	MtDNA
Penaeus japonicus (Bate, 1888) synonym of *Marsupenaeus japonicus*	Tsoi et al. 2007	Microsatellites
Mugil cephalus Linnaeus, 1758	Livi et al. 2011	MtDNA
Myripristis berndti Jordan and Evermann, 1903	Craig et al. 2007, Muths et al. 2011	MtDNA, Microsatellites
Naso brevirostris (Cuvier, 1829)	Horne et al. 2008	MtDNA
Naso vlamingii (Valenciennes in Cuvier and Valenciennes, 1835)	Klanten et al. 2007	MtDNA
Negaprion acutidens (Rüppell, 1837)	Schultz et al. 2008	MtDNA, Microsatellites
Nerita albicilla Linnaeus, 1758#	Crandall et al. 2008a	MtDNA
Nerita plicata Linnaeus, 1758#	Crandall et al. 2008a	MtDNA
Penaeus monodon Fabricius, 1798	Duda and Palumbi 1999, Mandal et al. 2012	Other nuclear markers, Microsatellites
Periclimenes soror Nobili, 1904	Crandall et al. 2008b	MtDNA
Perna viridis (Linnaeus, 1758)#	Prakoon et al. 2010, Yap et al. 2004	Microsatellites, Allozymes

Appendix 1. Continued.

Species name and authority	Citations for studies included in this data set	Marker
Phycomenes zostericola Bruce, 2008[#]	Haig et al. 2010	MtDNA
Pinctada maxima (Jameson, 1901)[#]	Lind et al. 2007	Microsatellites
Plectorhinchus flavomaculatus (Cuvier in Cuvier and Valenciennes, 1830)	Han et al. 2008	MtDNA
Plectroglyphidodon dickii (Liénard, 1839)	Fauvelot and Planes 2002	Allozymes
Plectropomus leopardus (Lacépède, 1802)	Van Herwerden et al. 2009b	MtDNA
Polynemus sheridani MacLeay, 1884[#] synonym of *Polydactylus macrochir* (Günther, 1867)	Chenoweth and Hughes 2003	MtDNA
Pomacentrus coelestis Jordan and Starks, 1901	Liu et al. 2008, Mirams et al. 2011	MtDNA
Pomacentrus moluccensis Bleeker, 1853	Drew et al. 2008	MtDNA
Pomacentrus pavo (Bloch, 1787)	10.1007/s00227-002-0869-7	Allozymes
Pristipomoides filamentosus (Valenciennes in Cuvier and Valenciennes, 1830)	Gaither et al. 2011b	MtDNA, Microsatellites
Pristipomoides multidens (Day, 1871)	Ovenden et al. 2002, Ovenden et al. 2004	MtDNA
Protoreaster nodosus (Linnaeus, 1758)[#]	Crandall et al. 2008b	MtDNA
Pterapogon kauderni Koumans, 1933	Bernardi and Vagelli 2004, Hoffman et al. 2005, Vagelli et al. 2009	MtDNA, Microsatellites
Pterocaesio chrysozona (Cuvier in Cuvier and Valenciennes, 1830)	Doherty et al. 1995	Allozymes
Scarus frenatus Lacepède, 1802	Dudgeon et al. 2000	MtDNA
Scarus ghobban Forsskål, 1775	Visram et al. 2010	MtDNA
Scarus psittacus Forsskål, 1775	Winters et al. 2010	MtDNA
Scarus rubroviolaceus Bleeker, 1847	Fitzpatrick et al. 2011	Microsatellites
Scylla serrata (Forsskål, 1775)	Fratini and Vannini 2002, Gopurenko and Hughes 2002, Gopurenko 1999	MtDNA
Sicyopterus aiensis Keith, Watson & Marquet, 2004[‡]	Lord et al. 2012	MtDNA
Sicyopterus lagocephalus (Pallas, 1770)	Hoareau et al. 2012, Lord et al. 2012	MtDNA
Sicyopterus sarasini Weber and de Beaufort, 1915	Lord et al. 2012	MtDNA
Siganus argenteus (Quoy and Gaimard, 1825)	Magsino and Juinio-Meñez 2008	Allozymes
Siganus fuscescens (Houttuyn, 1782)	Magsino and Juinio-Meñez 2008, Ravago-Gotanco and Juinio-Menez 2010	Allozymes, MtDNA

Appendix 1. Continued.

Species name and authority	Citations for studies included in this data set	Marker
Siganus guttatus (Bloch, 1787)	Iwamoto et al. 2009	MtDNA
Sinularia flexibilis (Quoy and Gaimard, 1833)[#]	Bastidas et al. 2001	Allozymes
Sphyraena barracuda (Edwards in Catesby, 1771)	Daly-Engel et al. 2012	MtDNA
Stegastes fasciolatus (Ogilby, 1889)	Ramon et al. 2008	MtDNA
Stegastes nigricans (Lacépède, 1802)	Doherty et al. 1995	Allozymes
Stegostoma fasciatum (Hermann, 1783)	Dudgeon et al. 2009	MtDNA, Microsatellites
Stichopus chloronotus Brandt, 1835[#]	Uthicke et al. 1999, Uthicke et al. 2001	Allozymes
Thyca crystallina (Gould, 1846)[#]	Crandall et al. 2008b, Kochzius et al. 2009	MtDNA
Tridacna crocea Lamarck, 1819[#]	DeBoer et al. 2008, Kochzius and Nuryanto 2008	MtDNA
Tridacna derasa (Röding, 1798)[#]	Macaranas et al. 1992	Allozymes
Tridacna gigas (Linnaeus, 1758)[#]	Benzie and Williams 1995	Allozymes
Tridacna maxima (Röding, 1798)[#]	Benzie and Williams 1997, Nuryanto and Kochzius 2009	Allozymes, MtDNA
Zebrasoma flavescens (Bennett, 1828)	Eble et al. 2011b	MtDNA, Microsatellites